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(71) Applicant *(for all designated States except US)*: **DECODE GENETICS EHF.** [IS/IS]; Sturlugötu 8, IS-101 Reykjavik (IS).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **MARTINEZ, Roger, Moraga, A.** [ES/DE]; Bleichstrasse 6, 60313 Frankfurt am Main (DE). **SIGURDSSON, Gunnar, Thor** [IS/IS]; Kjarrholmi 8, IS-200 Kopavogur (IS).

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(54) Title: NUCLEIC ACIDS ENCODING G PROTEIN-COUPLED RECEPTORS

(57) Abstract: Nucleic acids encoding G protein-coupled receptors are disclosed, and methods of using same.

NUCLEIC ACIDS ENCODING G PROTEIN-COUPLED RECEPTORS

RELATED APPLICATIONS

This application claims the benefit of and priority to U.S Provisional Application 60/301,095, filed June 26, 2001 and to U.S. Provisional Application 60/333,185, filed November 6, 2001, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

G protein-coupled receptors ("GPCRs") are a superfamily of intrinsic transmembrane cell-surface receptors that mediate the transmission of extracellular signals into the cell to produce a cellular response. There are thought to be anywhere from 400 to over 1000 different members of this family. GPCRs are intrinsic membrane proteins, and operate by a common transduction mechanism. In their inactive state, the GPCRs bind to the G proteins. Upon activation, they stimulate guanine nucleotide exchange on the G proteins, resulting in the release of GDP and the binding of GTP. The G-protein then dissociates from the GPCR, and interacts with the adenylate cyclases, which catalyze the conversion of ATP into cAMP. The cAMP then acts as a second messenger. The G proteins can cause intracellular coupling of the GPCRs with various intracellular enzymes, ion channels and transporters.

GPCRs (and perforce, G proteins) are involved in an enormous range of biological processes, and have been found to regulate such processes as hydrolysis of plasma membrane phospholipids, the K^+ and Ca^{2+} ion channels, yeast mating signals, the signaling by cholera and pertussis toxins, and proliferation in some cancers (*e.g.*, pituitary, adrenal, ovarian). The signal can be endogenous or exogenous or, in the case of rhodopsin receptors, the stimulus can be light. Many drugs bind to a GPCR and either produce a response or block the actions of the normal signal. The GPCR superfamily includes the cannabinoid and opioid receptors, chemokine, histamine, angiotensin, neurotensin, vasopressin, calcitonin, dopamine, glutamate and bombesin receptors, taste and odorant receptors, and many others.

SUMMARY OF THE INVENTION

The present invention relates to human G protein-coupled receptor (GPCR) genes, particularly nucleic acids comprising GPCR genes, and the amino acids

encoded by such nucleic acids. These sequences are shown in Tables I and II. In Tables I and II, each GPCR entry lists the name (*e.g.*, "MOOSE00162"), the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14797"), the exon locations (*e.g.*, "448003 . . 448092, . . ."), followed by the amino acid sequence and the nucleic acid sequence.

Sub-family information on the sequences is shown in Table III. For each sequence, the following information is provided: the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14797"), the name (*e.g.*, "MOOSE00162"), and the subfamily to which the sequence appears to belong. The assignments were made on the basis of the best E-value with which the sequence aligned. Sequences listed as "Class A Orphan" are those that have been characterized, and are known to bind GPCR-proteins.

In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention further relates to a nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention additionally relates to isolated nucleic acid molecules (*e.g.*, cDNA molecules) encoding a GPCR polypeptide (*e.g.*, encoding a polypeptide selected from the group consisting of SEQ ID NOs:1-124 (even numbers), as shown in Tables I and II).

The invention further provides a method for assaying a sample for the presence of a nucleic acid molecule comprising all or a portion of a GPCR in a sample, comprising contacting said sample with a second nucleic acid molecule comprising a nucleotide sequence encoding a GPCR polypeptide (*e.g.*, one of SEQ ID NOs:1-124 (odd numbers), as shown in Tables I and II, or the complement of one of SEQ ID NOs:1-124 (odd numbers); a nucleotide sequence encoding one of SEQ ID NOs:1-124 (even numbers), as shown in Tables I and II), or a fragment or derivative thereof, under conditions appropriate for selective hybridization. The invention additionally provides a method for assaying a sample for the level of expression of a GPCR polypeptide, or fragment or derivative thereof, comprising detecting (directly or indirectly) the level of expression of the GPCR polypeptide, fragment or derivative thereof.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention operatively linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method for preparing a polypeptide encoded by an isolated nucleic acid molecule described

herein (a GPCR polypeptide), comprising culturing a recombinant host cell of the invention under conditions suitable for expression of said nucleic acid molecule.

The invention further provides an isolated polypeptide encoded by isolated nucleic acid molecules of the invention (*e.g.*, GPCR polypeptide), as well as fragments or derivatives thereof. In a particular embodiment, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:1-124 (even numbers), as shown in Tables I and II. The invention also relates to an isolated polypeptide comprising an amino acid sequence which is greater than about 90 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-124 (even numbers), preferably about 95, 96, 97, 98 and 99 percent identical.

The invention also relates to an antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of the invention, as well as to a method for assaying the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, comprising contacting said sample with an antibody which specifically binds to the encoded polypeptide.

The invention further relates to methods of diagnosing a predisposition to a condition mediated by GPCRs. The methods of diagnosing such a predisposition in an individual include detecting the presence of a mutation in GPCR, as well as detecting alterations in expression of a GPCR polypeptide, such as the presence of different splicing variants of GPCR polypeptides. The alterations in expression can be quantitative, qualitative, or both quantitative and qualitative.

The invention additionally relates to an assay for identifying agents that alter (*e.g.*, enhance or inhibit) the activity or expression of one or more GPCR polypeptides. For example, a cell, cellular fraction, or solution containing a GPCR polypeptide or a fragment or derivative thereof, can be contacted with an agent to be tested, and the level of GPCR polypeptide expression or activity can be assessed. The activity or expression of more than one GPCR polypeptides can be assessed concurrently (*e.g.*, the cell, cellular fraction, or solution can contain more than one type of GPCR polypeptide, such as different splicing variants, and the levels of the different polypeptides or splicing variants can be assessed).

In another embodiment, the invention relates to assays to identify polypeptides that interact with one or more GPCR polypeptides. In a yeast two-hybrid system, for example, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also an GPCR polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the GPCR polypeptide, splicing

variant, or fragment or derivative thereof (*e.g.*, a GPCR polypeptide binding agent or receptor). Incubation of yeast containing both the first vector and the second vector under appropriate conditions allows identification of polypeptides which interact with the GPCR polypeptide or fragment or derivative thereof, and thus can be agents which alter the activity of expression of an GPCR polypeptide.

Agents that enhance or inhibit GPCR polypeptide expression or activity are also included in the current invention, as are methods of altering (enhancing or inhibiting) GPCR polypeptide expression or activity by contacting a cell containing GPCR and/or polypeptide, or by contacting the GPCR polypeptide, with an agent that enhances or inhibits expression or activity of GPCR or polypeptide.

Additionally, the invention pertains to pharmaceutical compositions comprising the nucleic acids of the invention, the polypeptides of the invention, and/or the agents that alter activity of GPCR polypeptide. The invention further pertains to methods of treating conditions mediated by GPCRs, by administering GPCR therapeutic agents, such as nucleic acids of the invention, polypeptides of the invention, the agents that alter activity of GPCR polypeptide, or compositions comprising the nucleic acids, polypeptides, and/or the agents that alter activity of GPCR polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to nucleic acids comprising G protein-coupled receptors ("GPCRs"), and the GPCR amino acids encoded by those nucleic acids.

The GPCR superfamily includes the receptors for many important signaling pathways, including, but not limited to, hormone receptors, growth factors, viral receptors, neuroreceptors, etc., such as acetylcholine, adrenocorticotropin (ACTH), adenosine, α-adrenergic receptors, β-adrenergic receptors, angiotensin, bombesin, bradykinin, C5a, calcitonin, cAMP, cannabinoid, C-C chemokine, cholecystokinin/gastrin (CCK/gastrin), cytomegalovirus, dopamine, endothelial differentiation gene-1, endothelin, formyl peptide, glutamate (metabotropic), gonadotropin-releasing hormone, growth hormone-releasing hormone, histamine, 5-hydroxytryptamine, interleukin-8, kinin, luteinizing hormone/follicle-stimulating hormone/thyroid-stimulating hormone (LH/FSH/TSH), mas, melanocortin, muscarinic, neuropeptide Y, neurotensin, odorant, opioid, opsins, parathyroid hormone, platelet-activating factor (PAF), prolactin, prostaglandin E, rhodopsins, secretin, serotonin, somatostatin, tachykinin, taste, testis specific, thrombin, thromboxine A_2, thyrotropin-releasing hormone (TRH), tyramine/octopamine, vasoactive intestinal peptide (VIP), vasopressin, viral and yeast mating factor.

These receptors are involved in the treatment of infections and various diseases and conditions, including, but not limited to, bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; cancers; diabetes; asthma; Parkinson's disease; both acute and congestive heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy (benign prostatic hyperplasia); chronic renal failure; renal disease; impaired glucose tolerance; seizure disorder; depression; anxiety; obsessive compulsive disorder; affective neurosis/disorder; depressive neurosis/disorder; anxiety neurosis; dysthymic disorder; behavior disorder; mood disorder; shizophrenia; psychosexual dysfunction; sex disorder; sexual disorder; disturbed biological and circadian rhythms; feeding disorders, such as anorexia, bulimia, cachexia, and obesity; Cushing's syndrome/disease; basophil adenoma; prolactinoma; hyperprolactinemia; hypopituitarism; hypophysis tumor/adenoma; hypothalamic diseases; Froehlich's syndrome; adenohypophysis disease; hypophysis disease; hypophysis tumor/adenoma; pituitary growth hormone; adenohypophysis hypofunction; adrenohpophysis hyperfuunction; hypothalamic hypogonadism; Kallman's syndrome (anosmia, hyposmia); functional or psychogenic amenorrhea; hypopituitarism; hypothalamic hypothyroidism; hypothalamic-adrenal dysfunctions; idiopathic hyperprolactinemia; hypothalamic disorders of growth hormone deficiency; idiopathic growth hormone deficiency; dwarfism; gigantism; acromegaly; disturbed biological and circadian rhythms; and sleep disturbances associated with such diseases as neurological disorders, heart and lung diseases, mental illness, and addictions; migraine; hyperalgesia; enhanced or exaggerated sensitivity to pain, such as hyperlgesia, causalgia and allodynia; acute pain; burn pain; atypical facial pain; neuropathic pain; back pain; complex regional pain syndromes I and II; arthritic pain; sports injury pain; pain related to infection, *e.g.*, HIV, post-polio syndrome, and post-herpetic neuralgia; phantom limb pain; labour pain; cancer pain; post-chemotherapy pain; post-stroke pain; post-operative pain; neuralgia; and tolerance to narcotics or withdrawal from narcotics; sleep disorders; sleep apnea; narcolepsy; insomnia; parasomnia; jet-lag syndrome; and other neurodegenerative disorders, which includes nosological entities such as disinhibition-dementia-parkinsonism-amyotrophy complex; pallido-ponto-nigral degeneration; and dyskinesias, such as Huntington's disease or Gilles dela Tourett's syndrome.

With the availability of complete genomic sequences for many organisms today, including *Homo sapiens*, it has become clear that there is a need for data mining techniques to extract the information in them, *e.g.*, gene prediction programs.

Of these, the most successful ones are those based on the comparison of known protein or protein-derived information, or those that use expressed sequence tags (ESTs) to predict gene location and structure.

One such algorithm is GeneWise. It bases its exon prediction on the use of Hidden Markov Models (HMMs) of proteins to be compared against a genomic sequence, so that the translation of the sequence will match the model in a similar way to other HMM profile searches (Eddy, *Curr. Opin. Struct. Biol.* 6(3):361-5, 1996), and allowing the presence of long insertions as long as they include donor and acceptor site sequences at both ends.

To take advantage of the algorithm, the models for different protein families must be built so that they represent the full-length sequences instead of the most common features in them. This is a major difference with existing HMM databases such as Pfam (Sonnhammer *et al.*, *Proteins* 28(3):405-20, 1997), in which each model is built to represent a family of proteins as broad as possible with minimum overlap between them.

In the present approach, the sequences were subdivided in several families so that the similarity inside of a group of them was over 50%. Given this approach, there are several points of overlap between different families when analyzing a sequence, so the discrimination must be done after the search is completed.

Several resources that include expert-supervised classifications are used to select the best groups of sequences, *e.g.*, the GPCR database (Horn *et al.*, *Nucleic Acids Res.* 26(1):275-9, 1998), PKR (Smith *et al.*, *Trends Biochem. Sci.* 22(11):444-6, 1997), NuclearRdb (Horn *et al.*, *Nucleic Acids Res.* 29:346-349, 2001), IOCH (Le Novere *et al.*, *Nucleic Acids Res.* 27(1):340-2, 1999), Enzyme (Bairoch, *Nucleic Acids Res.* 28:304-305, 2000) and Swiss-Prot (Bairoch *et al.*, *Nucleic Acids Res.* 28:45-48, 2000). When none is available, or the sequences included in some groups are too disrinatly related, the grouping must be done manually, using the ClustalW (Thompson *et al.*, *Nucleic Acids Res.* 22:4673-4680, 1994) package to measure the distance between different sequences.

The present model was built from multiple sequence alignments of the different protein families obtained with DiAlign 2 (Morgenstern, *Bioinformatics* 15(3):211-8, 1999). DiAlign works based on segment-to-segment comparisons instead of arbitrary thresholds for gap opening and extension, which makes it ideally suited for building models that represent an entire, full-length sequence, since the alignments built this way have more match states that would be assigned as insertion states when using other alignment algorithms. The models were built using the standard HMMer package.

To search for new genes, a genome-wide scan was done on the University of California at Santa Cruz sequences, using the GeneWise algorithm. It translates the genomic sequence on the fly to proteins and can therefore maintain a reading frame through insertions and deletions. The algorithm also rewards gaps in the genomic sequence relative to the model if they are encapsulated within introns, like splice structure.

For each superfamily of proteins, a classification was obtained in which the sequences are grouped by length and similarity. Each one of these groups was then used to build a HMM profile representing this group of sequences. This approach aims to have models that can represent the full length of the encoded proteins for a whole range of proteins, without being too specific for any one of them or being too general, as would be a HMM built for large groups of sequences. This classification was based either on existing expert-supervised classifications, or by retrieval of sequences and classification based on pairwise alignment distances.

These models were then searched against the October 2000 Fixed Release (with its subsequent corrections) and the April 2001 Fixed Release for data shown in Tables I and II, respectively, of the Santa Cruz contigs using the Paracel GeneMatcher+ Hardware Accelerator with the GeneWise algorithm. The sequences were chopped at 100 Kb with an overlap of 1 Kb. Each one of the superfamilies required between 3 and 6 days to complete and generate results. The results represent the coding regions of the complete final protein as it is found in the organism.

The cross-validation of the results was done in two steps. First, all of the hits with an E-value lower than 10^{-8} that did not overlap with one another were selected, and in the event of overlapping, the one with lowest E-value was selected. After selecting all of those matches, the DNA sequences were compared against the RefSeq database (Pruitt *et al.*, *Trends Genet.* 16(1): 44-47, 2000) using BLAST (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402, 1997).

Over 80% of the sequences were 90% or more identical to an existing human RefSeq entry and/or mRNA from GenBank. The differences are usually due to picking the wrong model for a certain sequence that appears as a hit more than once in different families, being a different valid splice variant, which can be tested by comparing to the EST database, or by addition of a small last exon to complete the match instead of accept an stop codon in a previous one. In all of such cases, the results are easily and quickly corrected by eye. Very rarely the algorithm will actually make a wrong prediction, which is consistent with the expected behaviour (Guigo *et al.*, *Genome Res.* 10(10): 1631-42, 2000).

Of the remaining sequences, over 50% have a match over 90% identical in the public domain protein databases, and the differences between those sequences in the databases and the potential translations is basically the same as the differences between the DNA sequences and the RefSeq entries.

The full sequences of the GPCR genes and splice variants are shown in Tables I and II as SEQ ID NOs:1-124 (odd numbers). The amino acids encoded by these nucleic acids are shown in Tables I and II as SEQ ID NOs:1-124 (even numbers).

A number of the genes were linked to markers known to be associated with human diseases genes. These are shown in Table IV. The diseases were linked to the HMM genes in the following manner: (1) the HMM gene models were compared to the consensus of the human genome sequence, located and the results kept in a relational database; (2) all possible markers (Sequence Tagged Sites (STS's)) (public or deCODE Genetics) are also located in the same consensus using ePCR or BLAT and results kept in a relational database; and (3) LOD scores for diseases are linked to markers. A span of one LOD drop around the marker was also given. A computer program takes each LOD peak and links it to the consensus through the markerhit in the database. The database is then queried for all HMM genes within the span of one LOD drop or a minimum of 15 Mb in each direction from the marker. The output is the name of the peak marker and its distance to the HMM gene.

NUCLEIC ACIDS OF THE INVENTION

Accordingly, the invention pertains to isolated nucleic acid molecules comprising human GPCR genes. The term, "GPCR", as used herein, refers to an isolated nucleic acid molecule selected from the group shown in Tables I and II, and consisting of SEQ ID NOs:1-124 (odd numbers), and also to a portion or fragment of the isolated nucleic acid molecule (*e.g.*, cDNA or the gene) that encodes GPCR polypeptide (*e.g.*, a polypeptide selected from the group shown in Tables I and II, and consisting of SEQ ID NOs:1-124 (even numbers)). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1-124 (odd numbers) or the complement of such a nucleic acid molecule.

The isolated nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be the coding, or sense, strand or the non-coding, or antisense, strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3'

and 5' sequences (including regulatory sequences, for example). Additionally, the nucleic acid molecule can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (*e.g.*, as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide

sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with chromosomes), or for detecting expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a GPCR polypeptide (*e.g.*, a polypeptide having an amino acid sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:1-124 (even numbers)), or another splicing variant of a GPCR polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules which comprise a sequence that is different from the naturally-occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a GPCR polypeptide of the present invention are also the subject of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a GPCR polypeptide. Such variants can be naturally-occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a GPCR polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a GPCR gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to designated sequences via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers). In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NOs:1-124 (even numbers) or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a GPCR.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (*e.g.*, under high stringency conditions). "Specific hybridization," as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (*e.g.*, when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, *e.g.*, conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (*i.e.*, 100%) complementary to the second, or the first and second may share some degree of complementarity which is less than perfect (*e.g.*, 70%, 75%, 85%, 90%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, 1998 and 2001), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*, room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent

mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556, 1991, and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, 1998 and 2001, which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize. Generally, doubling the concentration of SSC results in an increase in T_m of ~17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

The percent identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between

the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877, 1993. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402, 1997. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller *CABIOS* 4(1): 11-17, 1998. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (ACCELRYS, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5, 1994; and FASTA described in Pearson and Lipman *Proc. Natl. Acad. Sci. USA* 85:2444-8, 1988.

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the complement of such a sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence selected SEQ ID NOs:1-124 (even numbers), or

polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, which encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500, (1991).

Typically, a probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and more typically about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the complement of such a sequence, or a sequence encoding an amino acid sequence selected from SEQ ID NOs:1-124 (even numbers), or polymorphic variant thereof. In preferred embodiments, a probe or primer comprises 100 or fewer nucleotides, preferably from 6 to 50 nucleotides, preferably from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence, preferably at least 80% identical, more preferably at least 90% identical, even more preferably at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967, 1991; Eckert *et al.*, *PCR Methods and Applications*

1:17, 1991; PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560, 1989, Landegren *et al.*, *Science* 241:1077, 1988, transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874, 1990) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be radiolabelled and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs:1-124 (odd numbers) and/or the complement of one or more of SEQ ID NOs:1-124 (odd numbers), and/or a portion of one or more of SEQ ID NOs:1-124 (odd numbers), or the complement of one or more of SEQ ID NOs:1-124 (odd numbers) and/or a sequence encoding the amino acid sequences of one or more of SEQ ID NOs:1-124 (even numbers), or encoding a portion of one or more of SEQ ID NOs:1-124 (even numbers), and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate

derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers which are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (*e.g.*, reagent kits) for use in the screening and/or diagnostic assays described herein.

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1-124 (odd numbers) and the complements thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid sequence of SEQ ID NOs:1-124 (even numbers) or polymorphic variant thereof. The constructs comprise a vector (*e.g.*, an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of

vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel,

supra. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*), insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide

using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous GPCR gene, or an exogenous nucleic acid encoding a GPCR polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in BioTechnology* 2:823-829 and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein

can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by GPCRs ("GPCR polypeptides") and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*, other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the

complement of such a nucleic acid, or portions thereof, *e.g.*, SEQ ID NO:1-124 (even numbers), or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or a complement of such a sequence, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NOs:1-124 (even numbers), or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to one or more of SEQ ID NOs:1-124 (odd numbers), or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding one of SEQ ID NOs:1-124 (even numbers), a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

To determine the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent

to amino acid or nucleic acid "identity". The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, percent homology equals the number of identical positions/total number of positions times 100).

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising one of SEQ ID NOs:1-124 (odd numbers), or a complement of such a nucleic acid (*e.g.*, SEQ ID NOs:1-124 (even numbers), or other variants). However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example β-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *J. Mol. Recog.* 8:52-58 (1995) and Johanson *et al.*, *J. Biol. Chem.* 270:16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

The isolated polypeptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

In general, polypeptides of the present invention can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using art-recognized methods. The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the

corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a disease state. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided. Antibodies are also provided which bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The invention provides antibodies to the polypeptides and polypeptide fragments of the invention, *e.g.*, having an amino acid sequence of one of SEQ ID NOs:1-124 (even numbers) or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOs:1-124 (odd numbers), or a complement or another variant or portion thereof. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and $F(ab')_2$ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A

chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor *et al.* (1983) *Immunol. Today* 4:72), The EBV-hybridoma technique (Cole *et al.* (1985), *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (Eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, *e.g.*, *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *Surf*ZAP™ Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9:1370-1372 (1991);

Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Antibody detection can be facilitated by coupling it to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

DIAGNOSTIC AND SCREENING ASSAYS OF THE INVENTION

The present invention also pertains to a method of diagnosing or aiding in the diagnosis of a disease or condition associated with a GPCR gene or gene product in an individual. Diagnostic assays can be designed for assessing GPCR gene expression, or for assessing activity of GPCR polypeptides of the invention. In one embodiment, the assays are used in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or condition associated with a GPCR, or a defect in a GPCR. The invention also provides for prognostic (or predictive) assays for determining whether an

individual is susceptible to a disease of condition associated with a GPCR, *e.g.*, if an individual is at risk for addiction to an opoid. For example, mutations in the gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of symptoms associated with a susceptibility to a disease or condition associated with a GPCR. Another aspect of the invention pertains to assays for monitoring the influence of agents (*e.g.*, drugs, compounds or other agents) on the gene expression or activity of polypeptides of the invention, as well as to assays for identifying agents that bind to a polypeptides. These and other assays and agents are described in further detail in the following sections.

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to a disease or condition associated with a GPCR, as well as in kits useful for diagnosis of a susceptibility to a disease or condition associated with a GPCR.

In one embodiment of the invention, susceptibility to a disease or condition associated with a GPCR can be diagnosed by detecting a polymorphism in a GPCR as described herein. The polymorphism can be a mutation in a GPCR, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift mutation; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such mutation may be present in a single gene. Such sequence changes cause a mutation in the polypeptide encoded by a GPCR gene. For example, if the mutation is a frame shift mutation, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to a disease or condition associated with a GPCR can be a synonymous mutation in one or more nucleotides (*i.e.*, a mutation that does not result in a change in the polypeptide encoded by a GPCR gene). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of

the gene. A GPCR gene that has any of the mutations described above is referred to herein as a "mutant gene."

In a first method of diagnosing a susceptibility to a susceptibility to a disease or condition associated with a GPCR, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, Eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a "test sample") of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with a GPCR (the "test individual"). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a GPCR is present, and/or to determine which splicing variant(s) encoded by the GPCR is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a GPCR or contains a nucleic acid encoding a particular splicing variant of a GPCR. The probe can be any of the nucleic acid molecules described above (*e.g.*, the gene, a fragment, a vector comprising the gene, a probe or primer, etc.).

To diagnose a susceptibility to a disease or condition associated with a GPCR, a test sample containing a GPCR, is contacted with at least one nucleic acid probe to form a hybridization sample. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs:1-124 (odd numbers), or the complement thereof, or a portion thereof; or can be a nucleic acid encoding a portion of one of SEQ ID NOs:1-124 (even numbers). Other suitable probes for use in the diagnostic assays of the invention are described

above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a GPCR. "Specific hybridization", as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the GPCR in the test sample, then the GPCR has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the GPCR, or of the presence of a particular splicing variant encoding the GPCR and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR. For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a GPCR, or of the presence of a particular splicing variant encoded by a GPCR, and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al., Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Hybridization of the PNA probe to a GPCR is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

In another method of the invention, mutation analysis by restriction digestion can be used to detect a mutant gene, or genes containing a polymorphism(s), if the mutation or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a GPCR (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology, supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the mutation or polymorphism in the GPCR, and therefore indicates the presence or absence of this susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Sequence analysis can also be used to detect specific polymorphisms in a GPCR. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene, and/or its flanking sequences, if desired. The sequence of a GPCR, or a fragment of the gene, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the gene, gene fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the gene, cDNA (*e.g.*, one or more of SEQ ID NOs:1-124 (odd numbers), or a complement thereof, or a nucleic acid sequence encoding one of SEQ ID NOs:1-124 (even numbers) or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the GPCR indicates that the individual has a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in a GPCR, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to a GPCR, and that contains a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a GPCR can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the gene that are associated with a susceptibility to a

susceptibility to a disease or condition associated with a GPCR, a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a GPCR, and its flanking sequences. The DNA containing the amplified GPCR (or fragment of the gene) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified GPCR is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the GPCR, and is therefore indicative of a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a GPCR. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. No. 5,143,854 (see also PCT Application No. WO 90/15070) and Fodor *et al.*, PCT Publication No. WO 92/10092 and U.S. Pat. No. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. Nos. 5,384,261; the entire teachings of which are incorporated by reference herein.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, Published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified by well known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the

array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. In alternate arrangements, it will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein.

Other methods of nucleic acid analysis can be used to detect polymorphisms in a GPCR or variants encoding by a GPCR. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al. Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.*, U.S. Pat. No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al. Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al., Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al., Cell* 15:25 (1978); Geever, *et al., Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al., Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al., Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In another embodiment of the invention, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with a GPCR can also be made by examining expression and/or composition of a GPCR polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is

assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a GPCR, or for the presence of a particular variant encoded by a GPCR. An alteration in expression of a polypeptide encoded by a GPCR can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a GPCR is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant GPCR polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of a susceptibility to a disease or condition associated with a GPCR is made by detecting a particular splicing variant encoded by that GPCR, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a GPCR in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a GPCR. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a susceptibility to a disease or condition associated with a GPCR. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a susceptibility to a disease or condition associated with a GPCR. Various means of examining expression or composition of the polypeptide encoded by a GPCR can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a

DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by a mutant GPCR, or an antibody that specifically binds to a polypeptide encoded by a non-mutant gene, or an antibody that specifically binds to a particular splicing variant encoded by a GPCR, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or mutant GPCR, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-mutant gene. The presence of a polypeptide encoded by a polymorphic or mutant gene, or the absence of a polypeptide encoded by a non-polymorphic or non-mutant gene, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR, as is the presence (or absence) of particular splicing variants encoded by the GPCR gene.

In one embodiment of this method, the level or amount of polypeptide encoded by a GPCR in a test sample is compared with the level or amount of the polypeptide encoded by the GPCR in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the GPCR, and is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. Alternatively, the composition of the polypeptide encoded by a GPCR in a test sample is compared with the composition of the polypeptide encoded by the GPCR in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a susceptibility to a disease or condition associated with that GPCR.

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as decribed herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP

analysis), allele-specific oligonucleotides, antibodies which bind to mutant or to non-mutant (native) GPCR polypeptide, means for amplification of nucleic acids comprising a GPCR, or means for analyzing the nucleic acid sequence of a GPCR or for analyzing the amino acid sequence of a GPCR polypeptide, etc.

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as "screening assays") for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs:1-124 (odd numbers), or the complement thereof, or a nucleic acid encoding an amino acid having the sequence of one of SEQ ID NOs:1-124 (even numbers), or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a GPCR nucleic acid), and the contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, binding agents, antibodies, small molecules or other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides

described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, GPCR binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with GPCR binding agents (*e.g.*, G-proteins, other receptors associated with GPCRs, or other binding agents); or which alter posttranslational processing of the GPCR polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a GPCR polypeptide, a cell, cell lysate, or solution containing or expressing a GPCR polypeptide (*e.g.*, one of SEQ ID NOs:1-124 (even numbers), or another splicing variant encoded by a GPCR), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of GPCR activity is assessed (*e.g.*, the level (amount) of GPCR activity is measured, either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the GPCR polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a GPCR polypeptide. An increase in the level of GPCR activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) GPCR activity. Similarly, a decrease in the level of GPCR activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) GPCR activity.

In another embodiment, the level of activity of a GPCR polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters GPCR activity.

The present invention also relates to an assay for identifying agents which alter the expression of a GPCR gene (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, G-proteins, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a GPCR polypeptide (*e.g.*, a GPCR gene) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of GPCR expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the GPCR expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differ(s), by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of GPCR. Enhancement of GPCR expression indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of GPCR expression indicates that the agent is an antagonist of GPCR activity. In another embodiment, the level and/or pattern of GPCR polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters GPCR expression.

In another embodiment of the invention, agents which alter the expression of a GPCR gene or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the GPCR gene operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*,

the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the GPCR, as indicated by its ability to alter expression of a gene that is operably linked to the GPCR gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of GPCR activity. In another embodiment, the level of expression of the reporter in the presence of the agent to be tested, is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

Agents which alter the amounts of different splicing variants encoded by a GPCR (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a GPCR binding agent. For example, a cell that expresses a compound that interacts with a GPCR (herein referred to as a "GPCR binding agent", which can be a polypeptide or other molecule that interacts with a GPCR, such as a G-protein) is contacted with a GPCR in the presence of a test agent, and the ability of the test agent to alter the interaction between the GPCR and the GPCR binding agent is determined. Alternatively, a cell lysate or a solution containing the GPCR binding agent, can be used. An agent which binds to the GPCR or the GPCR binding agent can alter the interaction by interfering with, or enhancing the ability of the GPCR to bind to, associate with, or otherwise interact with the GPCR binding agent. Determining the ability of the test agent to bind to a GPCR or a GPCR binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I, ^{35}S, ^{14}C or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is

also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a GPCR or a GPCR binding agent without the labeling of either the test agent, GPCR, or the GPCR binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide. Thus, these receptors can be used to screen for compounds that are agonists for use in treating a susceptibility to a disease or condition associated with a GPCR or antagonists for studying a susceptibility to a disease or condition associated with a GPCR. Drugs could be designed to regulate GPCR activation that in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more GPCR polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more GPCR polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (*e.g.*, nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a GPCR polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the GPCR polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a GPCR polypeptide binding agent or G-protein). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the GPCR polypeptide or fragment or derivative thereof. Such polypeptides

may be useful as agents that alter the activity of expression of a GPCR polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either GPCR, the GPCR binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows GPCR or a GPCR binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a GPCR is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the

mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by a GPCR, or to alter expression of a GPCR, by contacting the polypeptide or the gene (or contacting a cell comprising the polypeptide or the gene) with the agent identified as described herein.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the polypeptides described herein; comprising polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:1-124 (even numbers)); and/or comprising other splicing variants encoded by a GPCR; and/or an agent that alters (*e.g.*, enhances or inhibits) GPCR gene expression or GPCR polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a G-protein), an agent that alters GPCR gene expression, or a GPCR binding agent or binding partner, fragment, fusion protein or prodrug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters GPCR polypeptide activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium

stearate, polyvinyl pyrollidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devises ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, *e.g.*, preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium,

potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms of a susceptibility to a disease or condition associated with a GPCR, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic and/or therapeutic) for a susceptibility to a disease or condition associated with a GPCR, using a GPCR therapeutic agent. A "GPCR therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) GPCR polypeptide activity and/or GPCR gene expression, as described herein (*e.g.*, a GPCR agonist or antagonist). GPCR therapeutic agents can alter GPCR polypeptide activity or gene expression by a variety of means, such as, for example, by providing additional GPCR polypeptide

or by upregulating the transcription or translation of the GPCR gene; by altering posttranslational processing of the GPCR polypeptide; by altering transcription of GPCR splicing variants; or by interfering with GPCR polypeptide activity (*e.g.*, by binding to a GPCR polypeptide), or by downregulating the transcription or translation of a GPCR gene. Representative GPCR therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a nucleic acid encoding a GPCR polypeptide or active fragment or derivative thereof, or an oligonucleotide; for example, one of SEQ ID NOs:1-124 (odd numbers), or a complement thereof, or a nucleic acid encoding one of SEQ ID NOs:1-124 (even numbers), or fragments or derivatives thereof);

polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:1-124 (even numbers), and/or other splicing variants encoded by a GPCR, or fragments or derivatives thereof);

other polypeptides (*e.g.*, G-proteins); GPCR binding agents; peptidomimetics; fusion proteins or prodrugs thereof; antibodies (*e.g.*, an antibody to a mutant GPCR polypeptide, or an antibody to a non-mutant GPCR polypeptide, or an antibody to a particular splicing variant encoded by a GPCR, as described above); ribozymes; other small molecules; and

other agents that alter (*e.g.*, enhance or inhibit) GPCR gene expression or polypeptide activity, or that regulate transcription of GPCR splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed.

More than one GPCR therapeutic agent can be used concurrently, if desired.

A GPCR therapeutic agent that is a nucleic acid is used in the treatment of a susceptibility to a disease or condition associated with a GPCR. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease, but also preventing or delaying the onset of the disease, and also lessening the severity or frequency of symptoms of the disease. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a GPCR polypeptide in an individual. For example, a GPCR therapeutic agent can be administered in order to upregulate or increase the expression or availability of the GPCR gene or of specific splicing variants of GPCR, or, conversely, to downregulate or decrease the expression or availability of the GPCR gene or specific splicing variants of the GPCR. Upregulation or increasing expression or availability of a native GPCR gene or of a particular splicing variant could interfere

with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native GPCR gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The GPCR therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a GPCR polypeptide, such as one of SEQ ID NOs:1-124 (odd numbers), or a complement thereof; or another nucleic acid that encodes a GPCR polypeptide or a splicing variant, derivative or fragment thereof, such as a nucleic acid encoding one of SEQ ID NOs:1-124 (even numbers)) can be used, either alone or in a pharmaceutical composition as described above. For example, a GPCR or a cDNA encoding a GPCR polypeptide, either by itself or included within a vector, can be introduced into cells (either *in vitro* or *in vivo*) such that the cells produce native GPCR polypeptide. If necessary, cells that have been transformed with the gene or cDNA or a vector comprising the gene or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native GPCR expression and activity, or have mutant GPCR expression and activity, or have expression of a disease-associated GPCR splicing variant, can be engineered to express the GPCR polypeptide or an active fragment of the GPCR polypeptide (or a different variant of the GPCR polypeptide). In a preferred embodiment, nucleic acid encoding a GPCR polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate

coprecipitation, mechanical techniques (*e.g.*, microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (*e.g.*, an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (*e.g.*, an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a GPCR is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the GPCR polypeptide, *e.g.*, by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA which encodes the GPCR polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the GPCR. In one embodiment, the oligonucleotide probes are modified oligonucleotides that are resistant to endogenous nucleases, *e.g.* exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.*, (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the GPCR. The antisense oligonucleotides bind to GPCR mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the

antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad Sci. USA* 84:648-652 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *Bio/Techniques* 6:958-976 (1988)) or intercalating agents. (See *e.g.*, Zon, *Pharm. Res.* 5: 539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells that express GPCR *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systemically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous GPCR transcripts and thereby prevent translation of the GPCR mRNA. For example, a vector can be introduced *in vivo* such that it is taken up in a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the

desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

Endogenous GPCR expression can be reduced by inactivating or "knocking out" GPCR or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, a mutant, non-functional GPCR (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous GPCR (either the coding regions or regulatory regions of GPCR) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the GPCR *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the GPCR. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-mutant GPCRs can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-mutant, functional GPCR, *e.g.*, a gene having one of SEQ ID NOs:1-124 (odd numbers), or the complement thereof, or a portion thereof, in place of a mutant GPCR in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a GPCR polypeptide variant that differs from that present in the cell.

Alternatively, endogenous GPCR expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a GPCR (*i.e.*, the GPCR promoter and/or enhancers) to form triple helical structures that prevent transcription of the GPCR in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.* 6(6): 569-84 (1991); Helene, C., *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the GPCR proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a GPCR mRNA or gene sequence) can be used to investigate the role of one or GPCR in developmental events, as well as the normal cellular function of the GPCRs in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other GPCR therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility to

a disease or condition associated with a GPCR. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

A combination of any of the above methods of treatment (*e.g.*, administration of non-mutant GPCR polypeptide in conjunction with antisense therapy targeting mutant GPCR mRNA; administration of a first splicing variant encoded by a GPCR in conjunction with antisense therapy targeting a second splicing encoded by a GPCR), can also be used.

The teachings of all publications cited herein are incorporated herein by reference in their entirety.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

Table I

MOOSE00162 ctg14797 448003..448091, 561616..561669, 625017..625027, 718931..719797, 720713..720771

MIQTISNVSEAVVQIIASQMPDGDNTDFRYFIYAVTYTVILVPGLIGNILALWV
FYGYMKETKRAVIFMINLAIADLLQVLSLPLRIFYYLNHDWPFGPGLCMFCFYLKYV
NMYASIYFLVCISVRRFWFLMYPFRFHDCKQKYDLYISIAGWLIICLACVLFPLLRTS
DDTSGNRTKCFVDLPTRNVNLAQSVVMMTIGELIGFVTPLLIVLYCTWKTVLSLQDK
YPMAQDLGEKQKALKMILTCAGVFLICFAPYHFSFPLDFLVKSNEIKSCLARRVILIFH
SVALCLASLNSCLDPVIYYFSTNEFKKSFLEQFRVIASTQEDHSSAEERISELEDRLLEN
IQSEETKEKRIKNNE **(SEQ ID NO: 2)**

atgattcagacaatcagtaatgttagtgaagcagtagtccaaatcatagcttctcaaatgccagatggagacaatacagatttt
cgatactttatttatgcagtgacatacactgtcattcttgtgccaggtctcatagggaatatattagccctgtgggtattctatggttatatgaa
agaaacaaaacgagctgtgatatttatgataaacttagccattgctgacttactacaagttctttccttgccactgaggatcttctactacttg
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cctggaagacggttttatcactgcaagataaatatcccatggcccaagatcttggagagaaacagaaagccttgaagatgattctaacct
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gacaggctacttgaaaatatacagtcagaggagacaaaagaaaaaagaataaaaaacaatgaa **(SEQ ID NO: 1)**

MOOSE00638 ctg16465 1516512..1517438, 1589966..1590028

KSVLLYTLSFIYIFIFVIGMIANSVVVWVNIQAKTTGYDTHCYILNLAIADLWV
VLTIPVWVVSLVQHNQWPMGELTCKVTHLIFSINLFGSIFFLTCMSVDRYLSITYFTN
TPSSRKKMVRRVVCILVWLLAFCVSLPDTYYLKTVTSASNNETYCRSFYPEHSIKEW
LIGMELVSVVLGFAVPFSIIAVFYFLLARAISASSDQEKHSSRKIIFSYVVVFLVCWLPY
HVAVLLDIFSILHYIPFTCRLEHALFTALHVTQCLSLVHCCVNPVLYSFINRNYRYEL
MKAFIFKYSAKTGLTKLIDASRAHTRMHTHTHAHMHTHIHSLS **(SEQ ID NO: 4)**

aaaagcgtcctgctctacacgctctccttcatttacattttcatcttcgtcatcggcatgattgccaactccgtggtggtctgggt
gaatatccaggccaagaccacaggctatgacacgcactgctacatcttgaacctggccattgccgacctgtgggttgtcctcaccatcc
cagtctgggtggtcagtctcgtgcagcacaaccagtggcccatgggcgagctcacgtgcaaagtcacacacctcatcttctccatcaa
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gcacagcagccggaagatcatcttctcctacgtggtggtcttccttgtctgctggctgccctaccacgtggcggtgctgctggacatctt
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ctgctgcgtcaaccctgtcctctacagcttcatcaatcgcaactacaggtacgagctgatgaaggccttcatcttcaagtactcggccaa
aacagggctcaccaagctcatcgatgcctccagagcacacacgcgcatgcacacacacacacatgcacacatgcacacacacatac
attctctttct **(SEQ ID NO: 3)**

MOOSE00693 ctg16008 12028107..12028186, 12152632..12153541

IPLKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSSTIIMLNLACTDLLYL
TSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHPMSCFSIH

KTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKWYNLILT
ATTFCLPLVIVTLCYTTIIHTLTHGLQTDSCLKQKARRLTILLLLAFYVCFLPFHILRVI
RIESRLLSISCSIENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQAVCSTVRCKVS
GNLEQAKKIMVSSSSSSHY HHHHHHHHHLHPDSQKI **(SEQ ID NO: 6)**

atcccactcaagatgcactacctccctgttatttatggcattatcttcctcgtgggatttccaggcaatgcagtagtgatatccac
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MOOSE00717 ctg16282 864967..865847, 878276..878384

FLALRLMVALAYGLVGAIGLLGNLAVLWVLSNCARRAPGPPSDTFVFNLALA
DLGLALTLPFWAAESALDFHWPFGGALCKMVLTATVLNVYASIFLITALSVARYWV
VAMAAGPGTHLSLFWARIATLAVWAAAALVTVPTAVFGVEGEVCGVRLCLLRFPSR
YWLGAYQLQRVVLAFMVPLGVITTSYLLLLAFLQRRQRRRQDSRVVARSVRILVAS
FFLCWFPNHVVTLWGVLVKFDLVPWNSTFYTIQTYVFPVTTCLAHSNSCLNPVLYCL
LRREPRQALAGTFRDLRAASCLRASSASRSSSARACSLSRSRASRLPASVARS **(SEQ ID NO: 8)**

ttcctagccctgaggctcatggttgccctggcctatgggcttgtgggggccattggcttgctgggaaatttggcggtgctgtg
ggtactgagtaactgtgcccggagagcccctggcccaccttcagacaccttcgtcttcaacctggctctggcggacctgggactggca
ctcactctcccctttgggcagccgagtcggcactggactttcactggcccttcggaggtgccctctgcaagatggttctgacggccact
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ggtgctggctttcatggtgcccttgggcgtcatcaccaccagctacctgctgctgctggccttcctgcagcggcggcaacggcggcgg
caggacagcagggtcgtggcccgctctgtccgcatcctggtggcttccttcttcctctgctggtttcccaaccatgtggtcactctctggg
gtgtcctggtgaagtttgacctggtgccctggaacagtactttctatactatccagacgtatgtcttccctgtcactacttgcttggcacaca
gcaatagctgcctcaaccctgtgctgtactgtctcctgaggcgggagccccggcaggctctggcaggcaccttcagggatctgcggg
cggccagctgccttcgagcctcttcggcctcacgctccagcagtgcccgggcctgctcactctcccggagccgggcctccaggctgc
cagcttcggttgcccgttct **(SEQ ID NO: 7)**

MOOSE00721 ctg16228 1520153..1520285, 1521083..1521207, 1522029..1522164, 1522413..1522612, 1522847..1523221

RAVDAWLVPLFFAALMLLGLVGNSLVIYVICRHKPMRTVTNFYIANLAATDV
TFLLCCVPFTALLYPLPGWVLGDFMCKFVNYIQQVSVQATCATLTAMSVDRWYVT
VFPLRALHRRTPRLALAVSLSIWVGSAAVSAPVLALHRLSPGPRAYCSEAFPSRALER
AFALYNLLALYLLPLLATCACYAAMLRHLGRVARAGAVRAKVSRLVAAVVLLFAA
CWGPIQLFLVLQALGPAGSWHPRSYAAYALKTWAHCMSYSNSALNPLLYAFLGSHF
RQAFRRVCPCAPRRPRRPRRPGPSDPAAPHAELLRLGSHPAPARAQK **(SEQ ID NO: 10)**

cgggccgtggacgcctggctcgtgccgctcttcttcgcggcgctgatgctgctgggcctggtggggaactcgctggtcatc
tacgtcatctgccgccacaagccgatgcggaccgtgaccaacttctacatcgccaacctggcggccacggacgtgaccttcctcctgt
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cgcctgtcacccgggccgcgcgcctactgcagtgaggccttccccagccgcgccctggagcgcgccttcgcactgtacaacctgct
ggcgctgtacctgctgccgctgctcgccacctgcgcctgctatgcggccatgctgcgccacctgggccgggtcgcccgcgcaggcg
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gcaggcgctgggccccgcgggctcctggcacccacgcagctacgccgcctacgcgcttaagacctgggctcactgcatgtc
ctacagcaactccgcgctgaacccgctgctctacgccttcctgggctcgcacttccgacaggccttccgccgcgtctgcccctgcgcg
ccgcgccgccccgccgccccgccggcccggaccctcggaccccgcagccccacacgcggagctgctccgcctggggtccca
cccggcccccgccagggcgcagaag **(SEQ ID NO: 9)**

MOOSE00741 ctg877 402877..402934, 519710..520656

AALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFNLSVSDLAF
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LQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNLIYSMCLT
LLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVLFTPYHV
MRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDMLM
NQLRHNFKSLTSFSRWAHELLLSFRENDSPSSPSSNGAITEVSHRT **(SEQ ID NO: 12)**

gctgccctggaaaagtactaccttccatttttatgggattgagttcgttgtgggagtccttggaaataccattgttgtttacggc
tacatcttctctctgaagaactggaacagcagtaatatttatctctttaacctctctgtctctgacttagcttttctgtgcaccctccccatgctg
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cagtgcactcaggtcgtcatcaactccttttacattgtgacacggcctttggcctttctgaacagtgtcatcaaccctgtcttctatttttcttttg
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MOOSE00766 ctg15378 1264081..1264142, 1351477..1351796, 1351914..1352461

NLPLQITLSAIMIFILFVSFLGNLVVCLMVYQKAAMRSAINILLASLAFADMLL
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NPYRAKVLIAVSWATSFCVAFPLAVGNPDLQIPSRAPQCVFGYTTNPGYQAYVILISL
ISFFIPFLVILPFQMSIDMGFKTRAFTTILILFAVFIVCWAPFTTYSLVATFSKHFYYQHN
FFEISTWLLWLCYLKSALNPLIYYWRIKKFHDACLDMMPKSFKFLPQLPGHTKRRIHF
THTHTHTHTHTHTHTQKHM **(SEQ ID NO: 14)**

aacttgcctcttcagatcacccttctgctataatgatattcattctgtttgtgtcttttcttgggaacttggttgtttgcctcatggttt
accaaaaagctgccatgaggtctgcaattaacatcctccttgccagcctagcttttgcagacatgttgcttgcagtgctgaacatgcccttt
gccctggtaactattcttactacccgatggatttttgggaaattcttctgtagggtatctgctatgttttctggttatttgtgatagaaggagta
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ccttgtggcaacattcagtaagcacttttactatcagcacaacttttttgagattagcacctggctactgtggctctgctacctcaagtctgc
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tg **(SEQ ID NO: 13)**

MOOSE00772 ctg78 1060263..1060374, 1105772..1106011, 1106507..1107105

SLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQI
SLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSY
PSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILS
VVSFIVIPLIVMIACYSVVFCAARRQHALLCYQCKAAKVIFIIIFSYVLSLGPYCFLAVL
AVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKQLNQQSS
SDSGSSSSSEDERPMRSHVKNGEVGRRRRH **(SEQ ID NO: 16)**

agcctggcccacggcatcatccgctcaaccgtgctggttatcttcctcgccgcctctttcgtcggcaacatagtgctggcgct
agtgttgcagcgcaagccgcagctgctgcaggtgaccaaccgttttatctttaacctcctcgtcaccgacctgctgcagatttc
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aagaccattaagaaggaaatccaggacatgctgaagaaacaactaaaccagcagtcttcatctgactctggctcctcctcctcttcaga
agatgaacgacccatgagatcccatgtgaagaatggtgaggttggcaggcggcggagacat **(SEQ ID NO: 15)**

MOOSE00775 ctg15540 14488015..14488239, 14488744..14488768, 14488985..14489082, 14491445..14491621, 14495389..14495435, 14499020..14499178, 14539721..14539940

PGRAKMALVLTGVLIFALALFGNALVFYVVTRSKTMRTVTNIFICSLALSDML
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KMKWQYTNRRAFTMLGVVWLVAVIVGSPMWHIKYDFLYEKEHICCLEEWTSPVHQ
KIYTTFILVILFLLPLMVMLILYSKIGYELWIKKRKKRAVIMMVTVVALFAVCWAPFH
VVHMMIEYSEFLSHVTPSMIFAIVQIIGFSNSICNPIVYAFMNENFKKNVLSAVCYCIV
NKTFSPAQRHGNSGITMMRKKAKFSLRENPVEET **(SEQ ID NO: 18)**

ccgggacgcgccaagatggccctcgtgctcaccggcgtgctcatattcgccctggcgctctttggcaatgctctggtgtttta
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aagcaaagttttccctcagagagaatccagtggaggaaacc **(SEQ ID NO: 17)**

MOOSE00779 ctg16537 5292218..5292340, 5438500..5438551, 5450751..5450956, 5450981..5451284, 5462460..5462773

FFAAKIVIGIALAGIMLVCGIGNFVFIAALTRYKKLRNLTNLLIANLAISDFLVA
IICCPFEMDYYVVRQLSWEHGHVLCASVNYLRTVSLYVSTNALLAIAIDRYLAIVHPL
KPRMNYQTASFLIALVWMVSILIAIPSAYFATETVLFIVKSQEKIFCGQIWPVDQQLY
YKSYFLFIFGVEFVGPVVTMTLCYARISRELWFKAIRKRLRCRRKTVLVLMCILTAYV
LCWAPFYGFTIVRDFFPTVFVKEKHYLTAFYVVECIAMSNSMINTVPFLYFWLRWGF
TIFLRLTLSQKKKKRRRRKRKRTESRDSNRYLYTHVPSSIIHSTPAW **(SEQ ID NO: 20)**

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gaagaagaagaaaaagaaaaagaactgaaagcagagactcaaacagatatttgtacactcatgttcctagcagcattattcacagcact
ccagc ctgg **(SEQ ID NO: 19)**

MOOSE00804 ctg30162 16180..16299, 37790..38066, 71494..71629, 82561..82975

SWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMYFLLTNLSIIDMSL
ASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSFDRYIAICKPLHYA
SVISPQVCVALVVASWIMGVMHSMTPFIEYLLIRVSFLHCLSLLTLLKNSWLQVRGF
VFGFCILFYCLSFTFSLLVSSYIIILVTVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFI
YVWPFTISPLDKFLAIFYTVFTPVLNPIIYTLRNRDMKAAVRKIRTSISHFRQRTDHLD
KNSAKKTTNTKRTLDHVDLPDSHRT **(SEQ ID NO: 22)**

tcctgggaactacagatgtttttctttatggtgttttcattgctttatgtggcaacaatggtgggtaacagcctcatagtcatcaca
gttatagtggaccctcacctacactctcctatgtatttcctgcttaccaatctttcaatcattgatatgtctcttgcttctttcgccaccccaaag
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agtaatattattctttggaccttgcatcttcatctatgtgtggccctttaccatctctcctttggataaatttcttgccatattttacactgttttcac
ccccgtcctaaaccccattatttatacactaaggaatagggatatgaaggctgccgtaaggaaaattaggacttcaatatctcactttcgg
caaaggacagatcatctagacaaaaattcagccaaaaaaacaacaaatacaaagcgcactctagatcatgtggacctaccagatagtc
acagaaca **(SEQ ID NO: 21)**

MOOSE00814 ctg15378 3973801..3973891, 3975545..3975625, 4023376..4023510, 4032595..4032652, 4060801..4060926, 4186201..4186358, 4227631..4227840, 4235835..4235929

SVVDTVILPSMIGIICSTGLVGNILIVFTIIRSRKKTVPDIYICNLAVADLVHIVG
MPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLT
RWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCLSNLLIFSKKYFISLIF
CIIFFISISFISALIFITFLLLFLEKQQQQKKKHTSQVMHLLLLSSTFLVSWIPRYFILFEAI
VNGSSLMIWLSVCLLLVYKNACDFCTIHYFDVKCVFRRNYRQLSKKKSHGSFVPTTQ
TESLSSTPTQHRKVVVFGLARPLWAT **(SEQ ID NO: 24)**

agtgtggtagatacagtcatcctcccttccatgattgggattatctgttcaacagggctggttggcaacatcctcattgtattcac
tataataagatccaggaaaaaaacagtccctgacatctatatctgcaacctggctgtggctgatttggtccacatagttggaatgccttttc
ttattcaccaatgggcccgaggggagagtgggtgtttgggggcctctctgcaccatcatcacatccctggatacttgtaaccaatttg
cctgtagtgccatcatgactgtaatgagtgtggacaggtactttgccctcgtccaaccatttcgactgacacgttggagaacaaggtaca
agaccatccggatcaatttgggcctttgggcagcttcctttatcctggcattgcctgtctgggtctactcgaaggtcatcaaatttaaagac
ggtgttgagagttgtttgtcaaatttgcttatctttcaaagaaatattttatttcttgatcttttgtattatttctttatttcaatttcatttatttctgct
ctgatctttattacatttcttctactattcttagaaaaacaacaacaacaaaaaaaaaaacacacgtcacaggtcatgcatctcctactcttgt
cttccacattccttgtaagttggattcctaggtattttattctctttgaagcaattgtgaatgggagttcactcatgatttggctctctgtttgtct
gttattggtgtataagaatgcttgtgatttttgcaccattcattattttgatgttaaatgtgtctttaggagaaattacagacaattgtcaaagaa

aaaaagccatggaagctttgtgcccacaacccaaacagaaagtttatcctccaccccaacccaacacaggaaagtggttgtttttggttt
ggccagaccactatgggctact **(SEQ ID NO: 23)**

MOOSE00818 ctg15907 32727057..32727450, 32800163..32800610,
32874979..32875093
WPHLEVVLFVVILIFYLITLIGNLFIIILSYLDSHLHTPMYFFLSNLSFLDLCYTT
SSIPQLLVNLWGPEKTISYAGCTVQLYFVLALGTAECVLLVVMSYDRYAAVCRPLH
YTVLMHPRFCRLLAAASWVTLHSSFTFWVPLCGHRLVDHFFCEVPALLRLSCVDTH
ANELTLMVMSSIFVLIPLILILTAYGAIARAVLSMQSTTGLQKVFRTCGAHLMVVSLF
FIPVMCMYLQPPSENSPDQGKFIALFYTVVTPSLNPLIYTLRNKHVKGAAKRLLGACR
PMQSQPRTVRSSFFDRKATGCEPGSCVRTPAAQTC **(SEQ ID NO: 26)**
tggcctcatctggaagtagttctctttgtggttatcttgatcttctacttgataacactgataggaaacctgttcatcatcatcctgt
catacctggactcccatctccacactcccatgtacttcttcctttcaaatctctcatttctggatctctgctacaccaccagctctatccctca
gttgctggtgaatctctgggggcccggaaaagaccatctcttatgctggttgtacagttca
actttactttgttctcgcactgggaaccgcagagtgtgtcctactggtggtgatgtcctatgatcgttatgcagctgtgtgtagacctttgca
ttacactgtcctcatgcaccctcgtttctgccgcttgttggctgcggcttcttgggtaacacttcattcctcctttacttttctgggtaccccttg
tggacatcgcctagtggatcacttcttctgtgaagttccagcacttctgcgtttatcatgtgttgacacccatgcaaatgagctgaccctcat
ggtcatgagctccatttttgttctcatacctctcattctgattctcactgcctatggtgccattgcccgggctgtactgagcatgcaatcaacc
actgggcttcagaaagtgtttaggacatgtggagcccatcttatggttgtatctctcttttcattccagtcatgtgcatgtatctccagccac
catcagaaaattctcctgatcagggcaagttcattgccctcttttatactgttgtcacaccgagtcttaatcctctaatctacactctcagaaa
caagcatgtaaaaggggcagcgaagagactattgggtgcctgccgccccatgcagagccagcccagaactgtgaggtcaagtttctt
tgatagaaaggcaacaggttgtgagcctggctcctgtgtgaggactccggcagcacagacttgt **(SEQ ID NO: 25)**

MOOSE00822 ctg14294 995965..996055, 1019834..1020641, 1219431..1219494
VRVVPRTVFFLFFFLFILVLVSNILTVIILSQLVARRQKSSYNYLLALAAADILV
LFFIVFVDFLLEDFILNMQMPQVPDKIIEVLEFSSIHTSIWITVPLTIDRYIAVCHPLKYH
TVSYPARTRKVIVSVYITCFLTSIPYYWWPNIWTEDYISTSVHHVLIWIHCFTVYLVPC
SIFFILNSIIVYKLRRKSNFRLRGYSTGKTTAILFTITSIFATLWAPRIIMILYHLYGAPIQ
NRWLVHIMSDIANMLALLNTAINFFLYCFISKRFRTMAAATLKAFFKCQKQPVQIQPF
KQISLSPTHTHTHTHTHTHTSKDT **(SEQ ID NO: 28)**
gttcgtgtcgtgccccgcaccgtgttttttttgtttttttttttgtttatttggttcttgtttcaaatatcttgacagtgatcatcctctcc
cagctggtggcaagaagacagaagtcctcctacaactatctcttggcactcgctgctgccgacatcttggtcctctttttcatagtgtttgt
ggacttcctgttggaagatttcatcttgaacatgcagatgcctcaggtccccgacaagatcatagaagtgctggaattctcatccatccac
acctccatatggattactgtaccgttaaccattgacaggtatatcgctgtctgccacccgctcaagtaccacacggtctcatacccagccc
gcacccggaaagtcattgtaagtgtttacatcacctgcttcctgaccagcatcccctattactggtggcccaacatctggactgaagacta
catcagcacctctgtgcatcacgtcctcatctggatccactgcttcaccgtctacctggtgccctgctccatcttcttcatcttgaactcaat
cattgtgtacaagctcaggaggaagagcaattttcgtctccgtggctactccacggggaagaccaccgccatcttgttcaccattacctc
catctttgccacactttgggccccccgcatcatcatgattctttaccacctctatggggcgcccatccagaaccgctggctggtacacatc
atgtccgacattgccaacatgctagcccttctgaacacagccatcaacttcttcctctactgcttcatcagcaagcggttccgcaccatgg
cagccgccacgctcaaggctttcttcaagtgccagaagcaacctgtacaaattcaacctttcaagcagatatctttaagtccaacacaca
cacacacacacacacacacacacacacacacacacacttctaaagacact **(SEQ ID NO: 27)**

MOOSE00826 ctg15968 677807..678430, 679388..679470, 683881..684142
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLSLG
HLLLAALDMPFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLA
VGFPLRYAGRLRPRYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEP
ERPRFAAFTATLHAVGFVLPLAVLCLTSLQVHRVARRHCQRMDTRRRHRATRKIGIA
IATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRPFRQV
LAGMVHRLLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHN **(SEQ ID NO: 30)**

atgggccccggcgaggcgctgctggcgggtctcctggtgatggtactggccgtggcgctgctatccaacgcactggtgct
gctttgttgcgcctacagcgctgagctccgcactcgagcctcaggcgtcctcctggtgaatctgtctctgggccacctgctgctggcgg
cgctggacatgcccttcacgctgctcggtgtgatgcgcgggcggacaccgtcggcgcccggcgcatgccaagtcattggcttcctgg
acaccttcctggcgtccaacgcggcgctgagcgtggcggcgctgagcgcagaccagtggctggcagtgggcttcccactgcgctac
gccggacgcctgcgaccgcgctatgccggcctgctgctgggctgtgcctggggacagtcgctggccttctcaggcgctgcacttggc
tgctcgtggcttggctacagcagcgccttcgcgtcctgttcgctgcgcctgccgcccgagcctgagcgtccgcgcttcgcagccttca
ccgccacgctccatgccgtgggcttcgtgctgccgctggcggtgctctgcctcacctcgctccaggtgcaccgggtggcacgcagac
actgccagcgcatggacacccggcgccgccaccgcgccaccaggaagattggcattgctattgcgaccttcctcatctgctttgcccc
gtatgtcatgaccaggctggcggagctcgtgcccttcgtcaccgtgaacgcccagtggggcatcctcagcaagtgcctgacctacag
caaggcggtggccgacccgttcacgtactctctgctccgccggccgttccgccaagtcctggccggcatggtgcaccggctgctgaa
gagaaccccgcgcccagcatccacccatgacagctctctggatgtggccggcatggtgcaccagctgctgaagagaaccccgcgc
ccagcgtccacccacaac **(SEQ ID NO: 28)**

MOOSE00829 ctg14145 39703..40567, 63946..64061

LEGIKHWIFIPFFFMYMVAISGNCFILIIIKTNPRLHTPMYYLLSLLALTDLGLC
VSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFDRFVAICHPLRYS
VIITGQQVVRAGLIVIFRGPVATIPIVLLLKAFPYCGSVVLSHSFCLHQEVIQLACTDTT
FNNLYGLMVVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVL
VFFVPMMGLSLVHRFGKHAPPAIHLLMANVYLFVPPMLNPIIYSIKTKEIHRAIIKLLE
CRSLRSQCNQLEERVSVMEDEMNEMKQEEKFREKRIKR **(SEQ ID NO: 32)**

ttggaaggcatcaaacactggattttcatccccttttttctttatgtacatggttgccatctcaggcaattgtttcattctgatcattatt
aagaccaaccctcgtctgcacacacccatgtactatctactatccttgctggccctcactgacctggggctgtgtgtgtccacgttgccca
ccactatggggatcttctggtttaactcccagagtatctactttggagcgtgtcaaatccagatgttctgcatccactctttttccttcatgga
gtcctcagtgctcctcatgatgtcctttgaccgctttgtggccatctgccaccctctgaggtattcggtcattatcactggccagcaagtgg
tcagagcaggcctaattgtcatcttccggggacctgtggccactatccctattgtcctcctcctgaaggcttttccctactgtggatctgtg
gtcctctcccactcattttgcctgcaccaggaagtgatacagctggcctgcacagataccaccttcaataatctgtatggactgatggtgg
tagttttcactgtgatgctggacctggtgctcatcgcactgtcctatggactcatcctgcacacagtagcaggcctggcctcccaagagg
agcagcgccgtgcctttcagacatgcaccgctcatctctgtgctgtgctagtattctttgtgcccatgatggggctgtccctggtgcaccg
ttttgggaagcatgccccacctgctattcatcttcttatggccaatgtctacctttttgtgcctcccatgcttaacccaatcatatacagcatta
agaccaaggagatccaccgtgccattatcaaactcctagaatgcagaagtctcaggagccaatgcaatcaactggaagaaagggtat
cagtgatggaagatgaaatgaatgaaatgaagcaagaagagaagtttagagaaaaaagaataaaaaga **(SEQ ID NO: 31)**

MOOSE00838 ctg14667 1435690..1435800, 1536739..1536780, 1544674..1544727, 1594182..1594286, 1597404..1597553, 1597578..1598087

HSTADLVLFSVVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFFLSQLSLMDL
MLVCTNVPKMAANFLSGRKSISFVGCGIQIGLFVCLVGSEGLLLGLMAYDRYVAISH
PLHYPILMNQRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHFFCEMLSLL
KLACVIFACCVFMLLFPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAFFFC
QLPYQILSHQVVCSFYWVILGHRCDKSSLQSSTVSLSFAVLNPILYGSVARSFRRRAG
ALLVCRKKPQNSSENFTFTPTSFLLSPYITHTHTHTHAHTHV **(SEQ ID NO: 34)**

cacagtactgctgaccttgtcctcttctccgtggttatggcggtcttcacagtggccctctgtgggaatgtcctcctcatcttcct
catctacatggaccctcaccttcacacccccatgtacttcttcctcagccagctctccctcatggacctcatgttggtctgtaccaatgtgc
caaagatggcagccaacttcctgtctggcaggaagtccatctcctttgtgggctgtggcatacaaattggcctctttgtctgtcttgtggga
tctgaggggctcttgctgggactcatggcttatgaccgctatgtggccattagccacccacttcactatcccatcctcatgaatcagagg
gtctgtctccagattactgggagctcctgggcctttgggataatcgatggcttgatccagatggtggtagtaatgaatttcccctactgtgg
cttgaggaaggtgaaccatttcttctgtgagatgctatccttgttgaagctggcctgtgtgatatttgcttgctgtgtcttcatgcttctcttccc
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ctgctcctcccacctgacagcttttttttttgccaactaccttaccaaatcctttcccatcaagttgtctgttcattttattgggtgattttgggg
catagatgtgacaaatcttcattgcaatcaagtacagtgtcactttcatttgcggttcttaatccaattctatatggcagcgtcgcccgctcct

ttcggcgcagggcgggagcccttcttgtgtgcagaaaaaaaccacagaatagctcagaaaatttcacttttacccccacttctttcctcct
ttctccttacatcacgcacacacacacacacacacatgcacacacacacgtc **(SEQ ID NO: 33)**

MOOSE00843 ctg15064 31780507..31780654, 31841187..31841254,
31873514..31873564, 31907740..31907833, 31923371..31923572, 31930354..31930411,
31940910..31940952, 31944453..31944599, 32115413..32115576
LCFLQTEQLITLWVLFVFTIVGNSVVLFSTWRRKKKSRMTFFVTQLAITVGFL
LDFLILFIMPLHFSLVYLFHYESSPDFWCLQSYFFCVVLLYASTYVLVSLSIDRYHAIV
YPMKFLQGEKQARVLIVIAWSLSFLFSIPTLIIFGKRTLSNGEVQCWALWPDDSYWTP
YMTIVAFLVYFIPLTIISIMYGIVIRTIWIKSKTYETAKIKAIKYSIIIILAFICCWSPYFLF
DILDNFNLLPDTQERFYASVIIQNLPALNSAINPLIYYSVSQKNKRKRKRRSRRKKKE
KERRRRKKRRRRKKKEGRRGGEGRGKKEEERRKE **(SEQ ID NO: 36)**
ctctgtttcttgcagactgagcaattgataactctgtgggtcctctttgtttttaccattgttggaaactccgttgtgcttttttccaca
tggaggagaaagaagaagtcaagaatgaccttctttgtgactcagctggccatcacagtgggatttttgttggactttctcatcctattcatt
atgcctcttcacttctctttggtctatctctttcactatgagagctcacctgatttttggtgcttacaaagctacttttttgtgttg
tgctgctctacgcctctacctacgtcctggtgtccctcagcatagacagataccatgccatcgtctaccccatgaagttccttcaaggaga
aaagcaagccagggtcctcattgtgatcgcctggagcctgtcttttctgttctccattcccaccctgatcatatttgggaagaggacactgt
ccaacggtgaagtgcagtgctgggccctgtggcctgacgactcctactggaccccatacatgaccatcgtggccttcctggtgtacttc
atccctctgacaatcatcagcatcatgtatggcattgtgatccgaactatttggattaaaagcaaaacctacgaaacagcaaaaatcaag
gctatcaagtatagcatcatcatcattcttgccttcatctgctgttggagtccatacttcctgtttgacattttggacaatttcaacctccttcca
gacacccaggagcgtttctatgcctctgtgatcattcagaacctgccagcattgaatagtgccatcaacccctcatctactactctgtttc
tcaaaaaaacaaaagaaagagaaaaagaagaagtaggaggaagaagaaggaaaaagaaagaagaagaaggaagaagagaagg
agaaggaagaagaaagaaggaagaagaggaggagaaggaagaggaaagaaggaagaagagaggaggaaggaa **(SEQ ID NO: 35)**

MOOSE00846 ctg15944 960216..961037, 988991..989137
NLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLSLLDVMF
SSVVAPKVIVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIIDHFICDLFQLLTLACT
DTHILGLLVTLNSGMMCVAIFLILIASYTVILCSLKSYSSKGRHKALSTCSSHLTVVVL
FFVPCIFLYMRPVVTHPIDKAMAVSDSIITPMLNPLIYTLRNAEDIREILRLMFRAPFCP
LFYFIFPGWSQNPELRSPSSASQSSGVTGVSHC **(SEQ ID NO: 38)**
aacctggagctgtggaaaatattttctgctgtgtttcttgtcatgtatgtagccacagtgctggaaaatctacttattgtggtaact
attatcacaagtcagagtctgaggtcacctatgtatttttttcttaccttcttgtccctttggatgtcatgttctcatctgtcgttgcccccaagg
tgattgtagacaccctctccaagagcactaccatctctctcaaaggctgcctcacccagctgtttgtggagcatttctttggtggtgtggg
gatcatcctcctcactgtgatggcctatgaccgctacgtggccatctgtaagcccctgcactacacgatcatcatgagtccacgggtgtg
ctgcctaatggtaggaggggcttgggtgggggggatttatgcacgcaatgatacaacttctcttcatgtatcaaataccccttctgtggtccta
atatcatagatcactttatatgtgatttgtttcagttgttgacacttgcctgcacggacacccacatcctgggcctcttagttaccctcaacag
tgggatgatgtgtgtggccatctttcttatcttaattgcgtcctacacggtcatcctatgctccctgaagtcttacagctctaaagggcggca
caaagccctctctacctgcagctcccacctcacggtggttgtattgttctttgtcccctgtattttcttgtacatgaggcctgtggtcactcac
cccatagacaaggcaatggctgtgtcagactcaatcatcacacccatgttaaatcccttgatctatacactgaggaatgcagaggacata
agagagatactgaggctgatgtttcgtgccccctttttgtccttatttttatttttattttccaggctggtctcaaaatcctgagctcaggtcgcc
ctcctcggcctcccaaagttctggagttacaggtgtgagccactgc **(SEQ ID NO: 37)**

MOOSE00855 ctg14333 2003002..2003122, 2024409..2025211
VHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLL
FLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIW
FKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDMVQAALIMG
VLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLY

WLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRQGRCLTLSTRFREN
SITRTAPRGKSTPRIQSPSTRPHILQ **(SEQ ID NO: 40)**

gtgcacacggcctacctggtgctgagctccctggccatgttcacctgcctgtgcgggatggcaggcaacagcatggtgatc
tggctgctgggctttcgaatgcacaggaaccccttctgcatctatatcctcaacctggcggcagccgacctcctcttcctcttcagcatgg
cttccacgctcagcctggaaacccagcccctggtcaataccactgacaaggtccacgagctgatgaagagactgatgtactttgcctac
acagtgggcctgagcctgctgacggccatcagcacccagcgctgtctctctgtcctcttccctatctggttcaagtgtcaccggcccag
gcacctgtcagcctgggtgtgtggcctgctgtggacactctgtctcctgatgaacgggttgacctcttccttctgcagcaagttcttgaaat
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accctctttgtctgggtgcggaggagctcccagcagtggcggcggcagcccacacggctgttcgtggtggtcctggcctctgtcctgg
tgttcctcatctgttccctgcctctgagcatctactggtttgtgctctactggttgagcctgccgcccgagatgcaggtcctgtgcttcagct
tgtcacgcctctcctcgtccgtaagcagcagcgccaaccccgtcatctacttcctggtgggcagccggaggagccacaggctgccca
ccagacaggggcggtgcctcacactgtcaacccgattccgtgagaactctatcacgagaacagcaccacgggggaaatccaccccc
aggatccaatcaccttccaccaggccacacatcctacaa **(SEQ ID NO: 39)**

MOOSE00861 ctg16279 54051..54182, 115058..115808, 116858..116925

PCVAGVIPVIYYSVLLGLGLPGDLLTAVALARLATRTRRPSYYYLLALTASDII
IQVVIVFAGFLLQGAVLARQVPQAVVRTANILEFAANHASVWIAILLTVDRYTALCH
PLHHRAASSPGRTRRAIAAVLSAALLTGIPFYWWLDMWRDTDSPRTLDEVLKWAHC
LTVYFIPCGVFLVTNSAIIHRLRRRGRSGLQPRVGKSTAILLGITTLFTLLWAPRVFVM
LYHMYVAPVHRDWRVHLALDVANMVAMLHTAANFGLYCFVSKTFRATFCSCCPS
CSAMGRSQLTATSSSRVQAVLLPQPPEELGLQARATT **(SEQ ID NO: 42)**

ccgtgtgtggctggcgtcatccctgtcatctactacagtgtcctgctgggcttggggctgcctggtgacctcctgaccgcagt
ggccctggcgcgccttgccaccaggaccaggaggccctcctactactaccttctggcgctcacagcctcggatatcatcatccaggtg
gtcatcgtgttcgcgggcttcctcctgcagggagcagtgctggcccgccaggtgccccaggctgtggtgcgcacggccaacatcctg
gagtttgctgccaaccacgcctcagtctggatcgccatcctgctcacggttgaccgctacactgccctgtgccacccccctgcaccatcg
ggccgcctcgtccccaggccggacccgccgggccattgctgctgtcctgagtgctgccctgttgaccggcatcccccttctactggtgg
ctggacatgtggagagacaccgactcacccagaacactggacgaggtcctcaagtgggctcactgtctcactgtctatttcatcccttgt
ggcgtgttcctggtcaccaactcggccatcatccaccggctacggaggaggggccggagtgggctgcagccccgggtgggcaaga
gcacagccatcctcctgggcatcaccacactgttcaccctcctgtgggcgccccgggtcttcgtcatgctctaccacatgtacgtggcc
cctgtccaccgggactggagggtccacctggccttggatgtggccaatatggtggccatgctccacacggcagccaacttcggcctct
actgctttgtcagcaagactttccgggccacttttgctcttgttgcccaagctgtagtgcaatggggcgatctcagctcactgcaacctcc
tcctcccgggttcaagcagttctcctgcctcagcctcccgaggagctgggactacaggcgcgtgccaccaca **(SEQ ID NO: 41)**

MOOSE00872 ctg18147 32565..32680, 45290..45647, 45666..46148

DPELKLIPFSLFLSMYLVTILGNLLILLAVISDSHLHTPMYFLLFNLSFTDICLTT
TTVPKILVNIQAQNQSITYTGCLTQICLVLVFAGLESCFLAVMAYDRYVAICHPLRYT
VLMNVHFWGLLILLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCELACSDTLINN
ILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMPSARGKYKAFSTCGCHLSVFSLFYGTAF
GVYISSAVAESSRITAVASVMYTVVPQMMNPFIYSLRNKEMKKALRKLIECLTLCFV
LFFSLRWSLSLSPRLECNGTTSAHCNFRLRV **(SEQ ID NO: 44)**

gacccagaactgaagttaatccctttcagcctgttcctgtccatgtacctggtcaccatcctggggaacctgctcattctcctg
gctgtcatctctgactcccacctccacaccccatgtacttccttctctttaatctctcctttactgacatctgtttaaccacaaccacagtccc
aaagatcctagtgaacatccaagctcagaatcagagtatcacttacacaggctgcctcacccagatctgtcttgtcttggtttttgctggct
tggaaagttgctttcttgcagtcatggcctacgaccgctatgtggccatttgccacccactgaggtacacagtcctcatgaatgtccatttc
tggggcttgctgattcttctctccatgttcatgagcactatggatgccctggttcagagtctgatggtattgcagctgtccttctgcaaaaac
gttgaaatccctttgttcttctgtgaactcgcctgttctgacaccctcatcaacaacatcctcatatatttttgcaagtagtgtatttggtgcaatt
cctctctctggaataattttctcttattctcaaatagtcacctctgttctgagaatgccatcagcaagaggaaagtataaagcgttttccacct
gtggctgtcacctctctgttttttccttgttctatgggacagcttttggggtgtacattagttctgctgttgctgagtcttcccgaattactgctgt

ggcttcagtgatgtacactgtggtccctcaaatgatgaaccccttcatctacagcctgagaaataaggagatgaagaaagctttgagga
aacttattgaatgcctgactctttgttttgttttgttttttttctctgagatggagtctttctctgtctcccaggctggagtgcaatggcacgacctc
ggctcactgcaacttccgcctccgggtt **(SEQ ID NO: 43)**

MOOSE00880 ctg15944 3962338..3962443, 4014447..4014532, 4029024..4029117, 4033619..4034316

ATEFQVLLFLLFLLLYLMILCGNTAIIWVVCTHSTLRTPMYFFLSNLSFLELCY
TTVVVPLMLSNILGAQKPISLAGCGAQMFFFVTLGSTDCFLLAIMAYDRYVAICHPL
HYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEINHFLCDVPPVLRL
ACADIRVHQAVLYVVSILVLTIPFLLICVSYVFITCAILSIRSAEGRRRAFSTCSFHLTV
VLLHFPPLQVHHFFKNSAPFKTLLIPFIQPFGYVNVIPMLNPLIYSLRNKEVKEALRKIL
NRAKTQVTQTHRETGSHIHRQTDGCRPRQTGRYLHRQTE **(SEQ ID NO: 46)**

gccactgaattccaggttcttctcttccttctcttcctcctctcttacttgatgatcctctgtggcaacacagccatcatctgggtg
gtgtgcacacacagcaccctccgcaccccgatgtatttcttcctgtccaacctgtctttcctggaactctgctacaccaccgtggtagtac
ccttgatgctttccaacattttgggggcccagaagcccatttcgttggctggatgtggggcccaaatgttcttctttgtcaccctcggcagc
acggactgtttcctcttggcgatcatggcctatgaccgctatgtggctatctgccacccgctgcactacaccctcatcatgacccgcgag
ctgtgcacgcagatgctgggtggggccctgggcctggccctcttcccctccctgcagctcaccgccttaatcttcaccctgccctttgc
ggccaccaccaggaaatcaaccacttcctctgcgatgtgcctcccgtcctgcgcctggcctgcgctgacatccgcgtgcaccaggct
gtcctctatgtcgtgagcatcctcgtgctgaccatccccttcctgctcatctgcgtctcctacgtgttcatcacctgtgccatcctgagcatc
cgttctgccgagggccgccgccgggccttctccacctgctccttccacctcaccgtggtcctgctgcactttc
ctcccctgcaggttcaccacttctttaaaaattctgctcctttcaaaaccctgctcattccttcatccagccatttgggtatgtgaatgtcatc
cccatgttgaatcccctcatctacagcctgaggaacaaggaagtgaaggaggccctgagaaaaattctcaatagagccaagacacag
gtgacacagacacatagagagactggtagtcacatacacaggcagacagatgggtgcaggcctaggcagacaggcagatatctgc
atagacagacagaa **(SEQ ID NO: 45)**

MOOSE00882 ctg15944 1984917..1985024, 2124131..2124428, 2127756..2127837, 2273894..2274344

DPQMEIIFFVVFLIVYLVNVVGNIGMIILITTDTQLHTPMYFFLCNLSFVDLGYS
SAIAPRMLADFLTNHKVISFSSCATQFAFFVGFVDAECYVLAAMAYGRFVAICRPLH
YSTFMSKQVCLALMLGSYLAGLVSLVAHTTLTFSLSYCGCCIYLKERAGHRKLNYSI
FFILFSLFFSLIIILISYIFILIAILRMRSAESRRKAFSTCGSHLVAVTVFYGTLFCMYVRP
PTDRSVEQSKVIAVFYTFVSPMLNPIIYSLRNKDVKQAFWKLIRRNKSMACGRVGKT
KCSERPEKDPSICSDSEIVAAVVKE **(SEQ ID NO: 48)**

gaccctcagatggagatcatcttcttcgtggtcttcctcatagtttacctggttaatgtagtggggaatattggtatgattatcctg
attacaacagacactcagcttcacacacccatgtatttttcctctgcaacctctcctttgttgacctgggctactcctcagccattgccccc
aggatgctggctgacttcctaacaaatcacaaagttatctccttctccagctgtgccacccagtttgcttttttgtaggttttgtggatgctg
agtgctatgtcctggcagccatggcctatggtcgttttgtggccatttgtcgacccctccactatagcaccttcatgtccaagcaggtctgc
ttggctctcatgctgggctcttacctggctggtctagtgagtttagtagcccacactaccctcaccttcagcctgagttactgtggttgctgc
atatatttaaaggaaagagcaggacatagaaaattaaattatagtatctttttatcctttttctttatttttctccctcatcataatcctcatctcc
tacatcttcattctcattgccatcctgaggatgcgttctgctgaaagtaggcgcaaagcgttctccacctgcgggtcccacctggtggca
gtgactgtgttttatggaaccctgttctgcatgtacgttagacctcccacggacaggtcagtggaacagtccaaagtcattgctgttttcta
cacttttgtaagccctatgttgaaccccatcatctatagtttgaggaacaaggatgtgaaacaagctttttggaaactgatcagaagaaac
aaaagcatggcctgtggcagggtgggaaagacaaaatgttcagagaggccagagaaagacccatccatttgcagcgacagtgaaat
tgtggctgctgttgtgaaggaa **(SEQ ID NO: 47)**

MOOSE00886 ctg15296 1927198..1927675, 1927700..1928051, 1949720..1949831

NSEVQRVLFVVFLLIYVVTVCGNMLIVVTITSSPTLASPVYFFLANLSFIDTFYS
SSMAPKLIADSLYEGRTISYECCMAQLFGAHFLGGVEIILLTVMAYDRYVAICKPLHN
TTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFCGPNVINHFAFACTNTYVIG

LLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRCKALSTCGAHFIVVALFFVPCI
FTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMRKLFTWQANIQIQEI
QRMPQRYSSRRATPRHINVRFTKVEMKE **(SEQ ID NO: 50)**

aactcagaggtacagagagttctctttgtggtctttttgctgatctatgtggtcacggtttgtggcaacatgctcattgtggtcact
atcacctccagccccacgctggcttcccctgtgtatttttttcctggccaacctatcctttattgacacctttttattcttcttctatggctcctaaa
ctcattgctgactcattgtatgaggggagaaccatctcttatgagtgctgcatggctcagctctttggagctcatttttgggaggtgttgag
atcattctgctcacagtgatggcttatgaccgctatgtggccatctgtaagcccctgcacaatactaccatcatgaccaggcatctctgtg
ccatgcttgtaggggtggcttggcttgggggcttcctgcattcattggttcagctcctcctggtcctttggttgcccttctgtgggcccaatg
tgatcaatcactttgcctttgcctgcaccaatacgtatgtcattggtctgctggtggttgccaacagtggtttaatctgcctgttgaacttcct
catgctggctgcctcctacattgtcatcctgtactccttgaggtcccacagtgcagatgggagatgcaaagccctctccacctgtggagc
ccacttcattgttgttgccttgttctttgtgccctgtatatttacttatgtgcatccattttctactttacctatagacaaaaatatggcattattttat
ggtattctgacacctatgttgaatccactcatttataccctgagaaatgaagaggtaaaaaatgccatgagaaagctctttacatggcagg
ccaacattcagattcaggaaatacagagaatgccacaaagatactcctcaagaagagcaactccaagacacataaatgtcagattcac
caaagttgaaatgaaggaa **(SEQ ID NO: 49)**

MOOSE00899 ctg17659 60714..60781, 124639..124720, 298068..298255, 298292..298925

DMESSFSFGVILAVLASLIIATNTLVAVAVLLLIHKNDGVSLCFTLNLAVADTL
IGVAISGLLTDQLSSPSRPTQKTLCSLRMAFVTSSAAASVLTVMLITFDRYLAIKQPFR
YLKIMSGFVAGACIAGLWLVSYLIGFLPLGIPMFQQTAYKGQCSFFAVFHPHFVLTLS
CVGFFPAMLLFVFFYCDMLKIASMHSQQIRKMEHAGAMAGALRTVSVLIGSFALSW
TPFLITGIVQVACQECHLYLVLERYLWLLGVGNSLLNPLIYAYWQKEFRNILLFCLTC
VSITSLRKKLFRCIHHVANFICIHMHTHTHTHTHTHTHT **(SEQ ID NO: 52)**

gacatggaatcatctttctcatttggagtgatccttgctgtcctggcctccctcatcattgctactaacacactagtggctgtggc
tgtgctgctgttgatccacaagaatgatggtgtcagtctctgcttcaccttgaatctggctgtggctgacaccttgattggtgtggccatctc
tggcctactcacagaccagctctccagcccttctcggcccacacagaagaccctgtgcagcctgcggatggcatttgtcacttcctccg
cagctgcctctgtcctcacggtcatgctgatcacctttgacaggtaccttgccatcaagcagcccttccgctacttgaagatcatgagtgg
gttcgtggccgggggcctgcattgccgggctgtggttagtgtcttacctcattggcttcctcccactcggaatccccatgttccagcagact
gcctacaaagggcagtgcagcttctttgctgtatttcaccctcacttcgtgctgaccctctcctgcgttggcttcttcccagccatgctcctc
tttgtcttcttctactgcgacatgctcaagattgcctccatgcacagccagcagattcgaaagatggaacatgcaggagccatggctgga
gctctccgtactgtgtctgttctcattgggagctttgctctatcctggacccccttccttatcactggcattgtgcaggtggcctgccagga
gtgtcacctctacctagtgctggaacggtacctgtggctgctcggcgtgggcaactccctgctcaacccactcatctatgcctattggca
gaaggagttccgtaacattctgctcttctgcctcacatgtgtctctattacctctttgagaaagaagctctttcgttgtattcaccatgtggcta
actttatatgtatacatatgcatacacacacacacacacacacacacacacacacacacaca **(SEQ ID NO: 51)**

MOOSE00930 ctg18867 3972483..3972607, 4167256..4168117

SQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLAD
LSLLLFSAPIRATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYA
SDPAKQVSIHNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEE
FMSMFGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLL
SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSE
EFREGLKDSILRIHFVCSSMRSSYSSVKVFLCDSSNSGTSSDSTSNARS **(SEQ ID NO: 54)**

tcccaggactggagaaccatcatcccggctctcttggtggctgtctgcctggtgggcttcgtgggaaacctgtgtgtgattgg
catcctccttcacaatgcttggaaaggaaagccatccatgatccactccctgattctgaatctcagcctggctgatctctcctcctgctgt
tttctgcacctatccgagctacggcgtactccaaaagtgtttgggatctaggctggtttgtctgcaagtcctctgactggtttatccacacat
gcatggcagccaagagcctgacaatcgttgtggtggccaaagtatgcttcatgtatgcaagtgacccagccaagcaagtgagtatcca
caactacaccatctggtcagtgctggtggccatctggactgtggctagcctgttacccctgccggaatggttctttagcaccatcaggca
tcatgaaggtgtggaaatgtgcctcgtggatgtaccagctgtggctgaagagtttatgtcgatgtttggtaagctctacccactcctggca

tttggccttccattatttttgccagcttttatttctggagagcttatgaccaatgtaaaaaacgaggaactaagactcaaaatcttagaaacc
agatacgctcaaagcaagtcacagtgatgctgctgagcattgccatcatctctgctctcttgtggctccccgaatgggtagcttggctgtg
ggtatggcatctgaaggctgcaggcccggccccaccacaaggtttcatagccctgtctcaagtcttgatgttttccatctcttcagcaaat
cctctcatttttcttgtgatgtcggaagagttcagggaaggcttgaaagattccatcttaagaatccactttgtttgctcatccatgagaagc
agttactcatctgttaaagttttcttatgcgatagcagcaattcaggcacatcatcagactccacttctaatgccaggtct (**SEQ ID NO: 53**)

MOOSE00941 ctg3235 477077..477375, 493498..493721, 494218..494258, 519487..519562, 557358..557534, 582821..582914, 612454..612496

CYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNAVSIYILNLVAADFL
FLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTERCLIKHCISALWPIWYH
CRRPTHLSAVLCALLWAPSLLLAFLEGYYCAFLFKIGDYSWFQTFDFITGTWLIFKFV
VLFYVPLKIMFCSEIGITSVSHRAQPTISLTHMVASYLGVMLLLFLICSLPLGIKWFLLF
WILVDFDIFLCHLQPVSDVLSSLNSSANPIIYFFMGSFRQRVFCCCCCCCCCCFTKFLL
GITFVSRRGGSHLHSGHSRHVPSHSRH (**SEQ ID NO: 56**)

tgctacaagcagaccctgagcttcacggggctgacgtgcatcgtttcccttgtcgcgctgacaggaaacgcggttgtgctct
ggctcctgggctgccgcatgcgcaggaacgctgtctccatctacatcctcaacctggtcgcggccgacttcctcttccttagcggccac
attatatgttcgccgttacgcctcatcaatatccgccatcccatctccaaaatcctcagtcctgtgatgacctttccctactttataggcctaa
gcatgctgagcgccatcagcaccgagcgctgcctcatcaaacactgcatatctgccctgtggcccatctggtaccactgccgtcgccc
cacacacctgtcagcagtcctgtgtgccctgctctgggccccgtccctgctgcttgccttcctggaaggttactactgtgcttttctgtttaa
gattggggactacagttggtttcagacatttgatttcatcacaggcacgtggctgatttttaaatttgtggttctcttctatgttcccctgaaaa
tcatgttctgttctgagattggaattacaagcgtgagccaccgcgcccagccgacaatctctttaacccatatggttgcatcatatctagga
gtaatgttgctgctcttccttatttgcagcctgccttaggcattaagtggttcctattattctggatcctcgtggattttgatatcttcctttgtca
tttgcaaccagtttcagatgtcctgtcctctcttaacagcagtgccaaccccatcatttacttcttcatgggctcctttaggcagcgtgttttt
gttgttgttgttgttgttgctgctgttgttttacaaaattcctgttaggaataacttttgtgtccaggcgcggtggctcacacctgcattccggc
cattccaggcatgtcccctcccattccaggcat (**SEQ ID NO: 55**)

MOOSE00981 ctg15907 42265065..42265689, 42265723..42265979, 42310781..42310870

ERLLRLISAGVCGLILLVGLSANGLMLLVVGRGPGSPHPLHSLTHSLMMNITP
SDLLFLACVVPVLLLSFLQHNWWLGPAICTISQATNTATTFCIFYSMVATALLRHVA
VARPDLAFPAGWGTLLLLCGAMWALGLTESLPNWLFQRVAVEEETAGAPKTQACL
LLLSPAGTSCYISLLGALAFLPCTLGLGCSFSHVGWLLWTQPQENIGLSLVVLVVFVL
MWGPCSMLGYVAAMGYLPATPAAFVASSLCTILAYSNCAVSPILCFYLSRPFQAGLR
DLFCRPMMARHPRGPGQQERDSVSNNKTKTKTHTHTHTHTHTHT (**SEQ ID NO: 58**)

gagcgactgctccgactcatctctgctggggtctgtggcctcatcctgctggtggggctgtcagctaatgggctcatgctgct
ggtggtgggccggggcccgggctccccccacccgctccactccctgacccacagcctcatgatgaacatcacgccatctgacctgct
cttcctggcctgcgtggtgcctgtgctgctgctgagcttcctgcagcacaactggtggctgggccctgccatctgcaccattagccagg
ccaccaacacagccaccacgttctgcatcttctatagcatggtggccacagctctcctgcgccatgtggctgtggcccggcctgacctg
gccttcccagccggctggggcaccctcttgctgctctgtggggccatgtgggccctgggccttacagaatccctgcccaactggctgtt
ccagagggtggcagtggaggaggagacagcgggggctcccaagacccaggcctgcctcttgctcctgagccctgctgggacctcc
tgctacatcagcctgctgggagccctggccttcctgccatgcacgctggggctgggctgctctttcagccacgtgggctggctcctgtg
gacccagccccaagagaacatagggctcagccttgtggtgctggtggtttttgtgctgatgtgggggccctgctccatgctgggttatgt
ggcagccatgggctacctgcctgccacaccggctgcttttgtggcctccagcctctgcaccatcctggcctactccaattgcgctgtca
gccctatcctctgcttctacctctcccgcccccttccaggcaggactcagggacctcttctgcaggccgatgatggccaggcatcccaga
ggtcctgggcaacaagagcgagactctgtctcaaataataaaacaaaaaccaaaacacacacacacacacacacacacacacacac
acacaca (**SEQ ID NO: 57**)

MOOSE00994 ctg17802 159288..159335, 297487..298009, 298142..298330, 313005..313117

SLALYNVFPFFFWLLFVGALLGNGALLVVVLRTPGLRDALYLAHLCVVDLLA AASIMPLGLLAAPPPGLGRVRLGPAPCRAARFLSAALLPACTLGVAALGLARYRLIV HPLRPGSRPPPVLVLTAVWAAAGLLGALSLLGPPPAPPPAPARCSVLAGGLGPFRPL WALLAFALPALLLLGAYGGIFVVAPLAVGQFAACWLPYGCACLAPAARAAEAEAA VTWVAYSAFAAHPFLYGLLQRPVRLALGRLSRLRSSWAVRTTSGSRLLRGPCSVLD QTLSSSGPSLAGSS **(SEQ ID NO: 60)**

tctttagcactctacaatgtctttccatttttttctggcttcttttgtgggggcactgctgggcaacggcgcgctgctggtcgtg gtgctgcgcacgccgggactgcgcgacgcgctctacctggcgcacctgtgcgtcgtggacctgctggcggccgcctccatcatgcc gctgggcctgctggccgcaccgccgcccgggctgggccgcgtgcgcctgggccccgcgccatgccgcgccgctcgcttcctctcc gccgctctgctgccggcctgcacgctcggggtggccgcacttggcctggcacgctaccgcctcatcgtgcacccgctgcggccagg ctcgcggccgccgcctgtgctcgtgctcaccgccgtgtgggccgcggcgggactgctgggcgcgctctccctgctcggcccgccg cccgcaccgccccctgctcctgctcgctgctcggtcctggctgggggcctcgggcccttccggccgctctgggccctgctggccttc gcgctgcccgccctcctgctgctcggcgcctacggcggcatcttcgtggtggcgccgctggccgtgggccaatttgcagcctgctgg ctgccttatggctgcgcgtgcctggcgcccgcagcgcgggccgcggaagccgaagcggctgtcacctgggtcgcctactcggcctt cgcggctcacccttcctgtacgggctgctgcagcgccccgtgcgcttggcactgggccgcctctctcgcctgaggagcagctgggc ggtgaggaccacatctggatcaagactgctcagaggcccttgcagtgtgcttgaccaaacgctgtcaagttcagggcccagcctggct gggtcctcc **(SEQ ID NO: 59)**

MOOSE01139 ctg12634 1689941..1690075, 1696196..1696364, 1729541..1729632, 1731449..1731515, 1744203..1744423, 1748034..1748243, 1777967..1778134, 1813481..1813504, 1865325..1865428, 1868201..1868336

THLPSASSQIPALEESCEAVEAREIMWFKTRQGQIAKQPCPAGTIGVSTYLCLA PDGIWDPQGPDLSNCSSPWVVNHITQKRSCRAYVQSEENFNPNCSFWSYSKRTMTGY WSTQGCRLLTTNKTHTTCSCNHLTNFAVLMAHVEHSDAVHDLLLDVITWVGILLSL VCLLICIFTFCFFRGLQSDRNTIHKNLCISLFVAELLFLIGINRTDQPIACAVFAALLHFF FLAAFTWMFLEGVQLYIMLVEVFESEHSRRKYFYLVGYGMPALIVAVSAAVDYRSY GTDKVCWLRLDTYFIWSFIGPATLIIMLNVIFLGIALYKMFHHTAILKPESGCLDNIKS WVIGAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRK EYGKCLRTHCCSGKSTESSIGSGKTSGSRTPGRYSTGSQVNN **(SEQ ID NO: 62)**

acacaccttccatcagcatcgtcccaaatcccagctctcgaagagagctgtgaggctgtggaagcccgagaaatcatgtgg tttaagactcgtcaaggacagatagcaaagcagccatgccctgcaggaactataggtgtatcaacttatctatgccttgctcctgatgga atttgggatccccaaggtccagatctcagcaactgttcttctccttgggtcaatcatataacacagaagcgctcttgcagagcctatgtcc agtcagaggaaaatttcaaccctaactgttcattttggagctactccaagcgtacaatgacaggttattggtcaacacaaggctgtcggct cctgacaacaaataagacacatactacatgctcttgtaaccacctaacaaattttgcagtactgatggcacatgtggaacacagtgatgc ggtccatgacctccttctggatgtgatcacgtgggttggaattttgctgtcccttgtttgtctcctgatttgcatcttcacattttgctttttccgg gggctccagagtgaccgtaacaccatccacaagaacctctgcatcagtctctttgtagcagagctgctcttcctgattgggatcaaccga actgaccaaccaattgcctgtgctgttttcgctgccctgttacatttcttcttcttggctgccttcacctggatgttcctggaggggtgcag ctttatatcatgctggtggaggtttttgagagtgaacattcacgtaggaaatacttttatctggtcggctatgggatgcctgcactcattgtg gctgtgtcagctgcagtagactacaggagttatggaacagataaagtatgttggctccgacttgacacctacttcatttggagttttatagg accagcaactttgataattatgcttaatgtaatcttccttgggattgctttatataaaatgtttcatcatactgctatactgaaacctgaatcagg ctgtcttgataacatcaagtcatgggttataggtgcaatagctcttctctgcctattaggattgacctgggcctttggactcatgtatattaat gaaagcacagtcatcatggcctatctcttcaccattttcaattctctacagggaatgtttatatttatttccattgtgtcctacagaagaaggt acgaaaagagtatgggaaatgcctgcgaacacattgctgtagtggcaaaagtacagagagttccattggttcagggaaaacatctggtt ctcgaactcctggacgctactccacaggctcacaggtaaacaat **(SEQ ID NO: 61)**

MOOSE01146 ctg15998 3076899..3076950, 3227362..3227381, 3254354..3254409, 3255136..3255184, 3257523..3257602, 3334521..3334629, 3354815..3354918,

3355747..3355867, 3358761..3358914, 3368419..3368485, 3370880..3370950, 3371577..3371604, 3415043..3415096, 3441342..3441468, 3442278..3442323, 3512965..3513101

HRRLKQENHLNPGGRGCMGLWGGGLCWVPTAPGSCGAPPGRLRCPDWFSA LSSTSMMSGPSLSLCCPHGPRCLQTGHWSPRMQATVSGEGVWSNHGCALTRGNLTY SVCRCTHLTNFAILMQLARGHQVALSSISYVGCSLSVLCLVATLVTFAVLSTIRNQRY HIHANLSFAVLVAQVLLLISFRLEPGTVSGRSSTPCQVMAVLLHYFFLSAFAWMLVE GLHLYSMVIKVFGSEDSKHRYYYGMGWGFPLLICIISLSFAMDSYGTSNNCWLSLAS GAIWAFVAPALFVIVVPNFVFLVETGPVLLTGLASQDPSVRSTQLTAKAAAVLLPILG TSWVFGVLAVNGCAVVFQYMFATLNSLQGLFIFLFHCLLNSEVQGLEELQKKWWG GDPELGISRKPLPSGAAGAGKGEHSQGLGGKSRA **(SEQ ID NO: 64)**

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SAFLK **(SEQ ID NO: 68)**

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QA **(SEQ ID NO: 70)**

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gccgcccgccgggggccaggcccccgcaccgcggcggcggcaggggcggtggcggcggggacgcggcggcgcccccagct
cgcggcggcggcggtggcgggaaggcgcggcccccctggcggcggcgcggctccctgcgagcccgggtgccagtgccgcgcg
cctatggtgagcgtgtccagcgagcgccacccgctctacaaccgcgtcaagacaggccagatcgctaactgcgcgctgccctgcca
caaccccttttcagccaggacgagcgcgccttcaccgtcttctggatcggcctgtggtcggtgctctgcttcgtgtccaccttcgccac
cgtctccaccttccttatcgacatggagcgcttcaagtacccggagcggcccattatcttcctctcggcctgctacctcttcgtgtcggtg
ggctacctagtgcgcctggtggcgggccacgagaaggtggcgtgcagcggtggcgcgccgggcgcgggggggcgctgggggcg
cgggcggcgcggcggcgggcgcgggcgcggcgggcgcgggcgcgggcggcccgggcgggcgcggcgagtacgaggagct
gggcgcggtggagcagcacgtgcgctacgagaccaccggccccgcgctgtgcaccgtggtcttcttgctggtctacttcttcggcatg
gccagctccatctggtgggtgatcttgtcgctcacatggttcctggcggccggtatgaagtggggcaacgaagccatcgccggctact
cgcagtacttccacctggccgcgtggcttgtgcccagcgtcaagtccatcgcggtgctggcgctcagctcggtggacggcgacccg
gtggcgggcatctgctacgtgggcaaccagagcctggacaacctgcgcggcttcgtgctggcgccgctggtcatctacctcttcatcg
gcaccatgttcctgctggccggcttcgtgtcccctcttccgcatccgctcggtcatcaagcaacaggacggccccaccaagacgcacaa
gctggagaagctgatgatccgcctgggcctgttcaccgtgctctacaccgtgcccgccgcggtggtggtcgcctgcctcttctacgag
cagcacaaccgcccgcgctgggaggccacgcacaactgcccgtgcctgcgggacctgcagcccgaccaggcacgcaggcccga
ctacgccgtcttcatgctcaagtacttcatgtgcctagtggtgggcatcacctcgggcgtgtgggtctggtccggcaagacgctggagt
cctggcgctccctgtgcacccgctgctgctgggccagcaagggcgccgcggtgggcgggggcgcg **(SEQ ID NO: 73)**

MOOSE01451 ctg17341 5903471..5903744, 5904206..5904356, 5910947..5911003, 5919010..5919127, 5934289..5934313, 5939959..5940053, 5941313..5941394, 5947946..5948017, 5948441..5948532

LARSSNPFEEKRHSGFLNFQLFCSGFSPSLCCQTGTFRSAEVFYCLLFSCALLT
DQKEKMALHFLFHQTLQLIHLELEKMILKNLFMPYWDVWHHQFQYANQILGKGLY
CFFRVFVFYSCSFVELAVSRDRATALQPGRQSETLSQKKKKRNATDFCMLSLCIEGT
YLQIIRAICCKPTATGPVPFTQCVTKGSFKAQWQETTYNLFTFCCLFLLPLTAMVICYS
RIVLSVIFSKFLAPAGEFALPRSFDNCPRVRLRALRLALLILLTFILCWTPYYLLGMWY
WFSPTMLTEVPPSLSHILFLLGLLNAPLDPLLYGAFTL **(SEQ ID NO: 76)**

ctggcaaggagcagcaatccttttgaggagaagaggcactctggttttttgaattttcagcttttctgctctggtttctccccatct
ttgtgctgtcagacagggacatttaggtctgcagaagttttctattgccttttgttcagctgtgccctgctcacagaccagaaggagaagat
ggctttacattttctttccatcagacacttcaactcatacatttggagctggaaaagatgattttaaaaaatcttttcatgccctattgggatgt
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gcttgcagtgagccgagatcgtgccactgcactccagcctgggcgacagagcgagactctgtctcaaaaaaaaaaaaaaaagaaatg
caactgatttttgcatgttgtctttgtgtattgaaggaacatacctccaaataataagagccatttgttgcaaacccacagccactggccca

gtccctttcactcagtgtgtcaccaaaggcagcttcaaggctcaatggcaagagaccacctataacctcttcaccttctgctgcctctttct
gctgccactgactgccatggtcatctgctatagccgcattgtcctcagtgttatattttctaaattcctagcccctgctggtgaatttgccctc
ccccgctcctttgacaattgtccccgtgttcgtctccgggccctgagactggccctgcttatcttgctgaccttcatcctctgctggacacc
ttattacctactgggtatgtggtactggttctcccccaccatgctaactgaagtccctcccagcctgagccacatccttttcctcttgggcct
cctcaatgctcctttggatcctctcctctatggggccttcaccctt **(SEQ ID NO: 75)**

MOOSE01609 ctg37 223820..223885, 415276..416383, 418102..418139
LGAVTTPVIPALGDAEAGRSSEVIVLHYNYTGKLRGARYQPGAGLRADAVVC
LAVCAFIVLENLAVLLVLGRHPRFHAPMFLLLGSLTLSDLLAGAAYAANILLSGPLTL
KLSPALWFAREGGVFVALTASVLSLLAIALERSLTMARRGPAPVSSRGRTLAMAAA
AWGVSLLLGLLPALGWNCLGRLDACSTVLPLYAKAYVLFCVLAFVGILAAICALYA
RIYCQVRANARRLPARPGTAGTTSTRARRKPRSLALLRTLSVVLLAFVACWGPLFLL
LLLDVACPARTCPVLLQADPFLGLAMANSLLNPIIYTLTNRDLRHALLRLVCCGRHS
CGRDPSGSQQSASAAEASGGLRRCLPPGLDGSFSGSERSSPQRDGLDTSGSTGSPACV
MKSCLLGKHK **(SEQ ID NO: 78)**
ctgggcgcagtgactacgcctgtaatcccagcacttggggacgccgaggcaggcaggtcatctgaggtcatcgtcctgca
ttacaactacaccggcaagctccgcggtgcgcgctaccagccgggtgccggcctgcgcgccgacgccgtggtgtgcctggcggtgt
gcgccttcatcgtgctagagaatctagccgtgttgttggtgctcggacgccacccgcgcttccacgctcccatgttcctgctcctgggca
gcctcacgttgtcggatctgctggcaggcgccgcctacgccgccaacatcctactgtcggggccgctcacgctgaaactgtcccccg
cgctctggttcgcacgggagggaggcgtcttcgtggcactcactgcgtccgtgctgagcctcctggccatcgcgctggagcgcagcc
tcaccatggcgcgcaggggcccgcgcccgtctccagtcgggggcgcacgctggcgatggcagccgcggcctggggcgtgtcg
ctgctcctcgggctcctgccagcgctgggctggaattgcctgggtcgcctggacgcttgctccactgtcttgccgctctacgccaaggc
ctacgtgctcttctgcgtgctcgccttcgtgggcatcctggccgctatctgtgcactctacgcgcgcatctactgccaggtacgcgccaa
cgcgcggcgcctgccggcacggcccgggactgcggggaccacctcgacccgggcgcgtcgcaagccgcgctcgctggccttgct
gcgcacgctcagcgtggtgctcctggcctttgtggcatgttggggccccctcttcctgctgctgttgctcgacgtggcgtgcccggcgc
gcacctgtcctgtactcctgcaggccgatcccttcctgggactggccatggccaactcacttctgaaccccatcatctacacgctcacca
accgcgacctgcgccacgcgctcctgcgcctggtctgctgcggacgccactcctgcggcagagacccgagtggctcccagcagtc
ggcgagcgcggctgaggcttccgggggcctgcgccgctgcctgcccccgggccttgatgggagcttcagcggctcggagcgctca
tcgccccagcgcgacgggctggacaccagcggctccacaggcagccccgcctgtgtgatgaaatcatgtcttttaggaaaacataag
(SEQ ID NO: 77)

MOOSE02359 ctg15037 7933711..7933760, 7963115..7963181, 7973661..7973682,
7983319..7983352, 7998114..7998223, 7999445..7999609, 8000036..8000207,
8000817..8001020, 8001339..8001472, 8003204..8003358
SPQAPGTWAAAWVPLPTVDVPDHAHYTLGTVILLVGLTGMLGNLTVIYTFCR
SRSLRTPANMFIINLAVSDFLMSFTQAPVFFTSSLYKQWLFGETGCEFYAFCGALFGIS
SMITLTAIALDRYLVITRPLATFGVASKRRAAFVLLGVWLYALAWSLPPFFGWSAYV
PEGLLTSCSWDYMSFTPAVRAYTMLLCCFVFFLPLLIIIYCYIFIFRAIRETGRALQTFG
ACKGNGESLWQRQRLQSECKMAKIMLLVILLFVLSWAPYSAVALVAFAGYAHVLTP
YMSSVPAVIAKASAIHNPIIYAITHPKYRSDAVASWQSRRLGVHLYPWSLVFCHPSEF
ENHNWSTRDVAPGHLMTEMETRVLSILSQ **(SEQ ID NO: 80)**
tctccgcaggcacctgggacttgggctgctgcctgggtccccctccccacggttgatgttccagaccatgcccactataccc
tgggcacagtgatcttgctggtgggactcacggggatgctgggcaacctgacggtcatctataccttctgcaggagcagaagcctccg
gacacctgccaacatgttcattatcaacctcgcggtcagcgacttcctcatgtccttcacccaggcccctgtcttcttcaccagtagcctct
ataagcagtggctctttggggagacaggctgcgagttctatgccttctgtggagctctctttggcatttcctccatgatcaccctgacggc
catcgccctggaccgctacctggtaatcacacgcccgctggccacctttggtgtggcgtccaagaggcgtgcggcatttgtcctgctg
ggcgtttggctctatgccctggcctggagtctgccacccttcttcggctggagcgcctacgtgcccgaggggttgctgacatcctgctc
ctgggactacatgagcttcacgccggccgtgcgtgcctacaccatgcttctctgctgcttcgtgttcttcctcctctgcttatcatcatcta
ctgctacatcttcatcttcagggccatccgggagacaggacgggctctccagaccttcggggcctgcaagggcaatggcgagtccct

gtggcagcggcagcggctgcagagcgagtgcaagatggccaagatcatgctgctggtcatcctcctcttcgtgctctcctgggctccc
tattccgctgtggccctggtggcctttgctgggtacgcacacgtcctgacaccctacatgagctcggtgccagccgtcatcgccaaggc
ctctgcaatccacaaccccatcatttacgccatcacccaccccaagtacaggtcagatgctgtggcttcctggcagtccagacgtcttgg
ggtacacttgtacccctggtccctggtgttctgccaccctagcgagtttgaaaaccacaactggagcaccagggatgttgccccaggc
cacctgatgacagaaatggagactagagtgttgtctatactaagccaa **(SEQ ID NO: 79)**

MOOSE02360 ctg15907 53482006..53482053, 53509199..53509251,
53519616..53519786, 53524954..53525124, 53528381..53528715, 53541306..53541470,
53636121..53636147, 53655914..53655948, 53805160..53805178, 53813699..53813772,
53992100..53992118

SLLKIQKISRTWWRVPSTDVSCLPMWGDFRAVSSELEILVLTIGIFIFFLVGILS
TFGNGYVLYMSSRRKKKLRPAEIMTINLAVCDLGISVVGKPFTIISCFCHRWVFGWIG
CRWYGWAGFFFGCGSLITMTAVSLDRYLKICYLSYGVWLKRKHAYICLAAIWAY
ASFWTTMPLVGLGDYVPEPFGTSCTLDWWLAQASVGGQVFILNILFFCLLLPTAVIV
FSYVKIIAKVKSSSKEVAHFDSRIHSSHVLEMKLTKVAMLICAGFLIAWIPYAVVSVW
SAFGRPDSIPIQLSVVPTLLAKSAAMYNPIIYQQNFSISNFRDSLAQSSVPWIQCCYYP
QESRGQLERVVESRDFVRMSAVSADLQKFQRN **(SEQ ID NO: 82)**

tctctactaaaaatacaaaaaattagtcggacgtggtggcgggtgcctagcacagatgtgagctgcttacctatgtggggag
acttcagggctgtgagtagtgaactcgaaatcttagttttaacgattggaatttttatttttttccttgtagggattctgtccacatttggaaatg
gatatgtcctttacatgtcttctagacgaaagaagaagctgagacccgctgaaataatgactatcaatttagcagtctgtgatctggggatt
tcagttgtaggcaagccgttcaccatcatctcttgcttttgtcaccgctgggtgtttggctggatcggctgccgctggtatggatgggctg
gatttttctttggctgtggaagccttatcaccatgactgctgtcagcctggatcgatatttgaaaatctgctatttatcttatggggtttggctg
aaaagaaagcacgcctacatctgcctggcagccatctgggcctatgcttccttctggaccaccatgcccttggtaggtctgggggacta
cgtacctgagcccttcggaacctcgtgcaccctggactggtggctggcccaggcctcggtagggggccaggttttcatcctgaacatc
ctcttcttctgcctcttgctcccaacggctgtgatcgtgttctcctacgtaaagatcattgccaaggttaagtcctcttccaaagaagtagct
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ggattccttatgcagtggtgtctgtggtcagcttttggaaggccagactccattcccatacagctcctgtggtgccaaccctacttgca
aaatctgcagcgatgtacaatcccatcatttaccaacaaaacttctcaatatcaaattttcgtgattccctagctcagagctcagtcccttgg
attcagtgctgttattatcctcaagagagcaggggacagctagaaagggttgtagaatcgagagattttgtgaggatgtcagcagttagc
gcagatctacaaaaattccagaggaat **(SEQ ID NO: 81)**

Table II

MOOSE02352 ctg12376 2508254..2508274, 2512637..2512697, 2596061..2596100,
2609217..2609251, 2697256..2697388, 2697901..2698120, 2702134..2702373,
2703765..2703914, 2704936..2705391, 2785876..2785900, 2796650..2796801

MSVVLQDTQTLTIDSNINSLLIVALLVTGITGMHHHARLILKLFVSKSSINFAD
FISQSSSASPGGVDYILHGSTVTFQHGQNLSFINISIIDDNESEFEEPIEILLTGATGGAV
LGRHLVSRIIIAKSDSPFGVIRFLNQSKISIANPNSTMILSLVLERTGGLLGEIQVNWET
VGPNSQEALLPQNRDIADPVSGLFYFGEGEGGVRTIILTIYPHEEIEVEETFIIKLHLVK
GEAKLDSRAKDVTLTIQEFGDPNGVVQFAPETLSKKTYSEPLALEGPLLITFFVRRVK
GTFGEIMVYWELSSEFDITEDFLSTSGFFTIADGESEASFDVHLLPDEVPEIEEDYVIQL
VSVEGGAELDLEKSITWFSVYANDDPHGVFALYSDRQSILIGQNLIRSIQINITRLAGT
FGDVAVGLRISSDHKEQPIVTENAERQLVVKDGATYKVDVFGTFYYSFISCTDGAVN
LTYIQIISKPIFSHYTDAYIFLHYSLLNTFLCDNSHFKISRK **(SEQ ID NO: 84)**

atgagtgttgttctgcaggatactcagacgttaacaatagactcaaacattaacagcctgctcatagttgccctgctggtaact
gggattacaggcatgcaccaccacgcccggctaattttaaaattatttgtaagtaaaagtagcataaactttgctgatttcatctctcagag
ctcctctgccagtcccggaggtgttgattacattttgcatggcagtacagtcacctttcagcatgggcaaaacttaagttttataaatatctc
catcattgatgacaatgaaagtgaatttgaggagcccattgaaattctactcactggagctactggaggagcggtccttgggcgccacc

tagtgagcagaatcataatagctaagagtgactctccctttggagttataaggtttctcaatcaaagcaaaatttctattgctaatcccaattc
cacaatgattttatcactggtgctggagcggactggaggactcttgggagagattcaggtgaactgggagacagtaggacccaactct
caagaagccttactgccacagaatagagacattgcagacccagtgagcgggttgttctattttggagaaggagaaggaggagtgaga
accataattctgacaatctatcctcatgaagaaattgaagttgaagagacattcattattaaacttcatcttgtgaaaggagaagctaaatta
gactccagagctaaagatgttacattaaccatacaagagtttggtgacccaaatggagttgttcagtttgctcctgaaactttgtctaagaa
gacttattcagagcctctggctctggaagggcccctgctcattaccttctttgtcagaagagtcaagggcacctttggagagattatggttt
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atctggagaagagtatcacatggttctctgtttatgcaaatgatgacccacatggagtatttgccctgtattcggatcgccagtcaatactta
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gatcataaagaacagccgattgttaccgaaaatgcagagaggcagctggtggtcaaagatggtgccacatataaagtggacgtgtttg
gaacctttattacagcttcatctcctgtactgatggagctgtaaatctaacatacatccagatcatttcaaagcctatttttctcactacaca
gatgcctatatatttcttcattacagccttttaaatacttttctctgtgataattcccactttaaaatttcgagaaag **(SEQ ID NO: 83)**

MOOSE01169 ctg13067 1981228..1981248, 1981792..1982139, 1984400..1984592, 1984626..1984712, 1985489..1985522, 1985564..1985647, 1985892..1985938, 1986646..1986768, 1988270..1988412, 1988754..1988824, 1989127..1989251, 1991650..1992536

GGGILFMLLFPSKIHLITYKVYFFFRFNFQRFRWMKAMIHMIKEINKRKDILPN
ITLGYQIFDTCFTISKSVEAVLVFLTGQEENRPNFRNSTGAFPAGIVGAGGSFLSVPAS
RILGLYYLPQVGYTSTCVILSDKYQFPSYLRVIASDKIQSKAVVKRIQHFHFLTLSPRL
ECSGAILAHGNLCLPVAGITGVCHHARLIFVFLVETGFCHVAQADGVSLCCHAGVYN
SPASAPLVAGTTGAHHHAQLIFVFLRYVTLLSLQKGQSCPNVFMHYLGEEYFQHREQ
HLLNPEARVAGTLEEQKRSQCGWKDLSIVYTYFCNVMYHNLAQRLVIFSMLFNSDL
LWKTQHMKILISKINIKGKYFLGFQDDSWNHRSFTSRNRPLPHSVCTDVCPPGTRKGI
RSEGEPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAQKSECVLKEVEYLAYDE
ALGFTLVILSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLFI
DKPHNWSCMAGQVTLALGFSLCLSCLLGKTSSLFLAYRISKSKTQLTSMHPLYRKIIV
LISVLAEIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMFGIDAFLALLCFL
TTFVARQLPDNYYEGKCITFGMLVFFIIWMSFVPVYLSTKGKFKMAVEIFAILASSHG
LLGCIFAPKCLIILLRPERNTSEI VCG **(SEQ ID NO: 86)**

gggggaggtattttatttatgctgcttttcccctcaaagatccacctaatcacctacaaagtctatttctttttcaggtttaactttca
gagattccgctggatgaaagccatgatccacatgatcaaggagattaataagaggaaggatattttgcccaacatcactctgggctatc
agatctttgatacctgttttaccatctccaaatcagtggaagcagtcttggtatttcttacagggcaggaagaaaacaggcccaattttaga
aacagcactggagcatttccggcaggaattgttggagcaggtggatcattcttatcagttcctgcttcaagaattctagggttatattatttg
cctcaggtgggctatacctctacctgcgtgattcttagtgacaaataccagtttccatcttatcttcgtgtaatagccagcgataagatcca
gtcgaaggctgtggtaaaacgtatccaacactttcactttctcactctgtcgcccaggctggagtgcagtggcgccatcctggctcatgg
caacctctgcctcccagtagctgggattacaggtgtgtgccaccatgccagactaatttttgtatttttagtagagacagggttttgccatgt
tgcccaggctgACGGAGTCTCGCTCTGTTGCCATGCTGGAGTATAcaattctcctgcctcagcccccct
agtagctgggactacaggcgcacaccaccacgctcagctaatttttgtatttttaagatatgtaacacttctgtcattgcagaaaggacag
agctgccctaatgtgttcatgcattatctaggggaagaatatttccagcacagggaacagcaccttctaaaccctgaggcgcgtgtggct
ggcactttggaggaacagaaaagaagtcaatgtggctggaaagacttatctattgtgtatacatacttctgtaatgttatgtaccataacct
agctcagagattggtaatattttctatgttatttaattcagatttactctggaaaactcaacatatgaaaattctgatttctaaaataaatataaa
gggaaaatatttttttaggctttcaagatgattcttggaatcataggtccttcacaagcaggaacagacctcttccccattcagtgtgtactga
tgtgtgtcctcctgggactcggaaggggattcgttcagagggagaaccaatatgctgctttgactccatcccatgtgctgatggacacgt
gtcacggaaaccaggtgaaagggagtgtgaacaatgtggtgaagactattggtcaaatgcacaaaagagcgagtgtgtgctgaaaga
ggtggaataccttgcttatgatgaggccctgggattcacacttgtcattctttctgtctttggggcatttgtggtcttggcagtcacagctgtg
tatgtgatacacaggcacactcccctggtgaacgccagtgactggcagctgggctttctcattcaggtttctctgatcatcatgctgctgtc
gtccatgcttttcattgacaagccacacaactggtcctgcatggctggccaggtcactctggcactgggcttttctctttgcctgtcttgcct

tcttggaaagactagttcactgtttttagcctacagaatttccaaatccaaaactcaacttacatccatgcaccccctttatcggaaaatcatt
gtgctaatctctgttctagcggagattggcatatgtacagcctacttgatattggaacctcccatggtatacaagaacatggaatctcaaaa
tacaaagatcattctgggatgcaatgaaatttccatagagtttttgtactcgatgtttggaattgatgccttcttagccttgctatgctttcttac
aacttttgtggctcgccagttaccagataattactatgaaggaaaatgcatcacctttgggatgcttgtctttttcatcatttggatgtcttttgt
ccctgtttatttgagcaccaaaggcaagttcaaaatggctgtggaaatatttgcaatcttggcatccagccatggcttgttgggttgtatatt
tgctcctaagtgcctcattattttgctgaggccagagaggaacaccagtgaaattgtttgtgga **(SEQ ID NO: 85)**

MOOSE00810 ctg13284 7238060..7238539, 7247370..7247453, 7258514..7258731, 7329591..7329682, 7438551..7438609

RLVLAAVETTVLVLIFAVSLLGNVCALVLVARRRRRGATACLVLNLFCADLL
FISAIPLVLAVRWTEAWLLGPVACHLLFYVMTLSGSVTILTLAAVSLERMVCIVHLQ
RGVRGPGRRARAVLLALIWGYSAVAALPLCVFFRVVPQRLPGADQVSAPLCISWDV
SFVTLNFLVPGLVIVISYSKILQIRVSQQDFRLFRTLFLLMVSFFIMWSPIIITILLILIQNF
KQDLVIWPSLFFWVVAFTFANSALNPILYNMTLRVFRHRVLEIRDKLWPLTILHKFSS
GTSLPLGHTHTQAHTHTHAHTHLHT **(SEQ ID NO: 88)**

cggctggtgctggccgcggtggagacaaccgtgctggtgctcatctttgcagtgtcgctgctgggcaacgtgtgcgccctg
gtgctggtggcgcgccgacgacgccgcggcgcgactgcctgcctggtactcaacctcttctgcgcggacctgctcttcatcagcgcta
tccctctggtgctggccgtgcgctggactgaggcctggctgctgggccccgttgcctgccacctgctcttctacgtgatgaccctgagc
ggcagcgtcaccatcctcacgctggccgcggtcagcctggagcgcatggtgtgcatcgtgcacctgcagcgcggcgtgcggggtc
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ccaggactggtcattgtgatcagttactccaaaatttacagatccgcgtgtcccagcaggacttccggctcttccgcaccctcttcctcct
catggtctccttcttcatcatgtggagccccatcatcatcaccatcctcctcatcctgatccagaacttcaagcaagacctggtcatctggc
cgtccctcttcttctgggtggtggccttcacatttgctaattcagccctaaaccccatcctctacaacatgacactcagagtcttcaggcac
agggtcctggagattagggacaaactttggcccctgacaattttgcataagttcagctctggcacaagtctaccattgggacatacacac
acacaggcacacacacacacacatgcacacacacacttgcacaca **(SEQ ID NO: 87)**

MOOSE01192 ctg14473 2193277..2193464, 2196762..2196915, 2197105..2197234, 2208484..2208612, 2213869..2213892, 2217011..2217047, 2219508..2219537, 2222803..2222949, 2223833..2223862, 2224187..2224215, 2281784..2281826, 2317525..2317642

MGSGISSESKESAKRSKELEKKLQEDAERDARTVKLLLLGAGESGK
STIVKQMKRIIQGKHYTSEESAAWSLSAWSNIHKSINLIHHINRTKNKNHMISSIEAEK
AFHKIQQPLMLKTLNKQERETISNLWSGVNIQNLYSYTEYLIPACTTSYLNDLDRITA
SGYVPNEQDVLHSRVKTTGIIETQFSFKDLHFRMFDVGGQRSERKKWIHCFEGVTCII
FCAALSAYDMVLVEDEEVNRMHESLHLFNSICNHKYFSTTSIVLFLNKKDIFQEKVT
KVHLSICFPEYTGPNTFEDAGNYIKNQFLDLNLKKEDKEIYSHMTCATDTQNVKFVF
DAVTDIIIKENLKDCGLF **(SEQ ID NO: 90)**

atgggaagtggaattagttcagagagcaaggagtcagccaaaagatcaaaagaactggagaaaaagcttcaggaggatg
ctgagcgagatgcaagaaccgtaaagctgctactattaggagcaggagaatctgggaaaagtactattgttaaacaaatgaagagaat
aatacagggaaaacattatacatcggaggaatctgctgcatggagcttgagtgcctggtcgaacatacacaaatcaataaacttaatcc
atcacataaacagaaccaagaacaaaaaccacatgattagctcaatagaagcagaaaaggccttccacaaaattcaacagcctttgat
gctaaaaactctcaataaacaagagagagagacgataagtaatctatggtcaggggttaatatccaaaatttatattcatacaccgaatat
ttaataccagcctgcacaacaagctaccttaatgatttagatagaataacagcatctgggtatgtgccaaatgaacaagatgttctccattc
tcgagtgaaaacgactggaatcattgaaactcaattctccttaaagacttgcacttcaggatgtttgatgtaggtggacagagatctgag
agaaagaagtggattcactgctttgaaggagttacatgcattatattttgtgctgcacttagtgcctatgacatggtcctcgtggaagacga
agaagtgaatagaatgcatgaaagccttcacctgttcaacagtatctgtaatcacaagtatttttcaacaacctccattgtcctgttcctcaa
caaaaaagatatctttcaagaaaaggtaaccaaggtgcatcttagtatctgctttccagaatacactgggccaaatacatttgaagatgca
ggaaactacatcaagaaccagtttctagacctgaatttaaaaaaagaagataaggaaatttattcccacatgacctgtgctactgacacc

caaaatgtcaagtttgtgtttgacgcagttacagatataataatcaaagagaatctaaaagactgtgggcttttc **(SEQ ID NO: 89)**

MOOSE05621 ctg15361 27306427..27307048, 27307103..27307314, 27309374..27309499

SPGSRVILYIVFGFGAVLAVFGNLLVMISILHFKQLHSPTNFLVASLACADFLV GVTVMPFSMVRTVESCWYFGRSFCTFHTCCDVAFCYSSLFHLCFISIDRYIAVTDPLV YPTKFTVSVSGICISVSWILPLMYSGAVFYTGVYDDGLEELSDALNCIGGCQTVVNQ NWVLTDFLSFFIPTFIMIILYGNIFLVARRQAKKIENTERKAAKTLGVTVVAFMISWLP YSIDSLIDAFMGFITPACIYEICCWCAYYNSAMNPLIYALFYPWFRKAIKKLRKCKVF REYENKTTRLGVVGHACNPSTLGGQGGWITRSKD **(SEQ ID NO: 92)**

tcgccgggatcccgggtgattctgtacatagtgtttggctttggggctgtgctggctgtgtttggaaacctcctggtgatgattt caatcctccatttcaagcagctgcactctccgaccaattttctcgttgcctctctggcctgcgctgatttcttggtgggtgtgactgtgatgc ccttcagcatggtcaggacggtggagagctgctggtattttgggaggagtttttgtactttccacacctgctgtgatgtggcattttgttact cttctctctttcacttgtgcttcatctccatcgacaggtacattgcggttactgacccccctggtctatcctaccaagttcaccgtatctgtgtca ggaatttgcatcagcgtgtcctggatcctgcccctcatgtacagcggtgctgtgttctacacaggtgtctatgacgatgggctggaggaa ttatctgatgccctaaactgtataggaggttgtcagaccgttgtaaatcaaaactgggtgttgacagattttctatccttctttatacctacctttt attatgataattctgtatggtaacatatttcttgtggctagacgacaggcgaaaaagatagaaaatactgagagaaaagcagctaaaacc ctgggggtcacagtggtagcatttatgatttcatggttaccatatagcattgattcattaattgatgcctttatgggctttataaccccctgcctg tatttatgagatttgctgttggtgtgcttattataactcagccatgaatcctttgatttatgctttatttttacccatggtttaggaaagcaataaaa aaactgagaaagtgcaaagtgtttagggaatatgaaaataaaacaactaggctgggcgtggtgggtcacgcctgtaatcccagcacttt gggaggccaaggcgggtggatcacaaggtcaaaagat **(SEQ ID NO: 91)**

MOOSE05712 ctg3235 322845..323688, 338849..338916

CYNQTLSFTVLTCIISLVGLTGNAVVLWLLGYRMRRNAVSIYILNLAAADFLF LSFQIIRLPLRLINISHLIRKILVSVMTFPYFTGLSMLSAISTERCLSVLWPIWYRCRRPT HLSAVVCVLLWGLSLLFSMLEWRFCDFLFSGADSSWCETSDFIPVAWLIFLCVVLCV SSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGILGALIYRMHLNLEVLYCH VYLVCMSLSSLNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDKPEVDKASATRS RTRTTSTSSASTPPRPT **(SEQ ID NO: 94)**

tgctacaatcagaccctgagcttcacggtgctgacgtgcatcatttcccttgtcggactgacaggaaacgcggttgtgctctg gctcctgggctaccgcatgcgcaggaacgctgtctccatctacatcctcaacctggccgcagcagacttcctcttcctcagcttccagat tatacgtttgccattacgcctcatcaatatcagccatctcatccgcaaaatcctcgtttctgtgatgacctttccctactttacaggcctgagt atgctgagcgccatcagcaccgagcgctgcctgtctgttctgtggcccatctggtaccgctgccgccgccccacacacctgtcagcgg tcgtgtgtgtcctgctctggggcctgtccctgctgtttagtatgctggagtggaggttctgtgacttcctgtttagtggtgctgattctagttg gtgtgaaacgtcagatttcatcccagtcgcgtggctgatttttttatgtgtggttctctgtgtttccagcctggtcctgctggtcaggatcctct gtggatcccggaagatgccgctgaccaggctgtacgtgaccatcctgctcacagtgctggtcttcctcctctgcggcctgccctteggc attctgggggccctaatttacaggatgcacctgaatttggaagtcttatattgtcatgtttatctggtttgcatgtccctgtcctctctaaacag tagtgccaaccccatcatttacttcttcgtgggctcctttaggcagcgtcaaaataggcagaacctgaagctggttctccagagggctct gcaggacaagcctgaggtggataaagcatctgcaacgaggagccggacgagaaccacctcaacctcatccgcgtcaacgccacca aggcctacg **(SEQ ID NO: 93)**

MOOSE05732 ctg3235 1189276..1189408, 1206579..1207366

CGKETLIPVFLILFIALVGLVGNGFVLWLLGFRMRRNAFSVYVLSLAGADFLF LCFQIINCLVYLSNFFCSISINFPSFFTTVMTCAYLAGLSMLSTVSTERCLSVLWPIWYR CRRPRHLSAVVCVLLWALSLLLSILEGKFCGFLFSDGDSGWCQTFDFITAAWLIFLFM VLCGSSLALLVRILCGSRGLPLTRLYLTILLTVLVFLLCGLPFGIQWFLILWIWKDSDV LFCHIHPVSVVLSSLNSSANPIIYFFVGSFRKQECSLSCLSKQKSPTLLSERDFWIAVIA

EVSRGRRHEGFTLSFLG **(SEQ ID NO: 96)**

tgtggcaaggagaccctgatcccggtcttcctgatccttttcattgccctggtcgggctggtaggaaacgggtttgtgctctg
gctcctgggcttccgcatgcgcaggaacgccttctctgtctacgtcctcagcctggccggggccgacttcctcttcctctgcttccagatt
ataaattgcctggtgtacctcagtaacttcttctgttccatctccatcaatttccctagcttcttcaccactgtgatgacctgtgcctaccttgc
aggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgccgccccagaca
cctgtcagcggtcgtgtgtgtcctgctctgggccctgtccctactgctgagcatcttggaagggaagttctgtggcttcttatttagtgatg
gtgactctggttggtgtcagacatttgatttcatcactgcagcgtggctgatttttttattcatggttctctgtgggtccagtctggccctgctg
gtcaggatcctctgtggctccaggggtctgccactgaccaggctgtacctgaccatcctgctcacagtgctggtgttcctcctctgcggc
ctgccctttggcattcagtggttcctaatattatggatctggaaggattctgatgtcttattttgtcatattcatccagtttcagttgtcctgtcat
ctcttaacagcagtgccaaccccatcatttacttcttcgtgggctcttttaggaagcaggagtgctcactctcctgtttaagcaagcagaag
tctcccaccctcctttcagagagagacttctggattgcagttattgctgaagtaagccgaggaagaagacacgaggggttcacactttcc
tttttaggc **(SEQ ID NO: 95)**

MOOSE05740 ctg3235 274265..275065, 285148..285258

CYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNAVSIYILNLVAADFL
FLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRRPR
YLSSVMCVLLWALSLLRSILEWMFCDFLFSGANSVWCETSDFITIAWLVFLCVVLCG
SSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFC
HVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLDSMCRRTALYKTIRSRESYSL
SREQQREDPTHDSILS **(SEQ ID NO: 98)**

tgctacaagcagaccctgagcttcacggggctgacgtgcatcgtttcccttgtcgcgctgacaggaaacgcggttgtgctct
ggctcctgggctgccgcatgcgcaggaacgctgtctccatctacatcctcaacctggtcgcggccgacttcctcttccttagcggccac
attatatgttcgccgttacgcctcatcaatatccgccatcccatctccaaaatcctcagtcctgtgatgacctttccctactttataggcctaa
gcatgctgagcgccatcagcaccgagcgctgcctgtccatcctgtggcccatctggtaccactgccgccgccccagatacctgtcatc
agtcatgtgtgtcctgctctgggccctgtccctgctgcggagtatcctggagtggatgttctgtgacttcctgtttagtggtgctaattctgtt
tggtgtgaaacgtcagatttcattacaatcgcgtggctggttttttatgtgtggttctctgtgggtccagcctggtcctgctggtcaggattc
tctgtggatcccggaagatgccgctgaccaggctgtacgtgaccatcctcctcacagtgctggtcttcctcctctgtggcctgccctttgg
cattcagtgggccctgttttccaggatccacctggattggaaagtcttattttgtcatgtgcatctagtttccattttcctgtccgctcttaaca
gcagtgccaaccccatcatttacttcttcgtgggctcctttaggcagcgtcaaaataggcagaacctgaagctggacagcatgtgcagg
agaacggccctttataaaaccatcagatctcgtgagagttattcactatcacgagaacagcagagggaagacccaacccatgattcaat
actttcc **(SEQ ID NO: 97)**

MOOSE05748 ctg4256 14884996..14885118, 14904164..14905015

HSPTHTFLFFLVLAIFSVAFMGNSVMVLLIYLDTQLHTPMYFLLSQLFLMDLM
LICSTVPKMAFNYLSGSKSISMAGCATQIFFYVSLLGSECFLLAVMSYDRYIAICHPLR
YTNLMRPKICGLMTAFSWILGSMDAIIDAVATFSFSYCGSREIAHFFCDFPSLLILSCN
DTSIFEKVLFICCIVMIVFPVAIIIASYARVILAVIHMGSGEGRRKAFTTCSSHLMVVG
MYYGAGLFMYIRPTSDRSPMQDKLVSVFYTILTPMLNPLIYSLRNKEVTRALRKVRG
APLERKHSDSGFSTSSRSTGCATFSLCAHLRATSSAEV **(SEQ ID NO: 100)**

cacagccccacccacaccttcctcttctttctggtcctggccatcttttcagtggccttcatgggaaactctgtcatggttctcct
catctacctggacacccagctccacacccccatgtacttcctcctcagtcaactgttcctcatggacctcatgctcatctgctctaccgtac
ccaagatggccttcaactacttgtctggcagcaagtccatttctatggctggttgtgccacacaaattttcttctatgtatcactgcttggctc
cgaatgctttctgttggctgttatgtcttatgaccgctatattgccatttgccaccctctaagatacaccaatctcatgagacccaaa
atttgtggacttatgactgccttctcctggatcctgggctctatggatgcaatcattgatgctgtagcgacattttccttctcctactgtgggtc
tcgggaaatagcccacttcttctgtgacttcccttccctactaatcctctcatgcaatgacacatcaatatttgaaaaggttcttttcatctgct
gtatagtaatgattgtttttcctgttgcaatcatcatcgcttcctatgctcgagttattctggctgtcattcacatgggatctggagagggtcgt
cgcaaagcttttactacctgttcctctcacctcatggtggtgggaatgtactatggagcaggtttgttcatgtacatacggcccacatctga
tcgctcccctatgcaggacaagctggtgtctgtattctacaccatcctcactcccatgctgaatcccctcatctacagcctccgcaacaag

gaggtgaccagagcactcaggaaagtgagaggagccccgctggaaaggaaacattcggactccggtttcagcacctcctccagaa gcacaggatgtgcgaccttcagcctttgtgcccacctccgagccaccagctccgcagaagta **(SEQ ID NO: 99)**

MOOSE05757 ctg30162 475149..475607, 475650..476006, 490932..491042

RWELQIFFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGNLSFLDMCL STATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLLIIMAFDRYVAICKPLH YRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNLACIETYTLELFVIADSGL LSFTCFILLLVSYIVILVSVPKKSSHGLSKALSTLSAHIIVVTLFFGPCIFIYVWPFSSLAS NKTLAVFYTVITPLLNPSIYTLRNKKMQEAIRKLRFQYNSSPSKTFPQTRRRDKDYPR KTRAKEFHYHQIFFIRN **(SEQ ID NO: 102)**

cgatgggaacttcaaattttcttctttgtgacattttccctgatctacggtgctactgtgatgggaaacattctcattatggtcaca gtgacatgtaggtcaacccttcattctcccttgtactttctccttggaaatctctctttttggacatgtgtctctccactgccacaacacccaa gatgatcatagatttgctcactgaccacaagaccatctctgtgtggggctgcgtgacccagatgttcttcatgcacttctttgggggtgctg agatgactcttctgataatcatggcctttgacaggtatgtagccatatgtaaacccctgcactataggacaatcatgagccacaagctgct aaaggggtttgcgatactttcatggataattggttttttacactccataagccagatagttttaacaatgaacttgcctttctgtggccacaat cttgcttgcattgaaacatacaccctggaattatttgtcattgctgacagcgggctgctctctttcacctgtttcatcctcttgcttgtttcttac attgtcatcctggtcagtgtaccaaaaaaatcatcacatgggctctccaaggcgctgtccacattgtctgcccacatcattgtggtcactct gttctttggaccttgtatttttatctatgtttggccattcagtagtttggcaagcaataaaactcttgccgtattttatacagttatcacaccctta ctgaatccgagtatttataccctgagaaataagaaaatgcaagaggccataagaaaattacggttccaatataatagttcacccagcaaa actttccctcagacacgaagaagagataaagactatcccagaaaaacaagagctaaggaatttcattaccaccaaatctttttataagaa ac **(SEQ ID NO: 101)**

MOOSE05798 ctg13495 208823..208941, 209823..210141, 210181..210672

SQDIQLLVFVLILIFYLIILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFLDASYSFIV APRMLVDFLSEKKVISYRGCITQLFFLHFLGGGEGLLLVVMAFDRYIAICRPLHCSTV MNPRACYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVRQLLMVFNSG LMTLLCFLGLLASYAVILCHVRRAASEGKNKAMSTCTTRVIIILLMFGPAIFIYMCPFR ALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLIRCLVLCRLMTQTHTRSG LRNRKFIRQEGREELPHTEGEA **(SEQ ID NO: 104)**

tctcaagatattcagctcttggtctttgtgctgatcttaattttctaccttatcatcctccctggaaattttctcattattttcaccataa ggtcagaccctgggctcacagccccctctatttatttctgggcaacttggccttcctggatgcatcctactccttcattgtggctcccagg atgttggtggacttcctctctgagaaaaaggtaatctcctacagaggctgcatcactcagctctttttcttgcacttccttggaggagggga gggattactccttgttgtgatggcctttgaccgctacatcgccatctgccggcctctgcactgttcaactgtcatgaaccctagagcctgct atgcaatgatgttggctctgtggcttgggggttttgtccactccattatccaggtggtcctcatcctccgcttgcctttttgtggcccaaacc agctggacaacttcttctgtgatgtccgacagcttctaatggtcttcaacagtggcctgatgacactcctgtgctttctggggcttctggctt cctatgcagtcatcctctgccatgttcgtagggcagcttctgaagggaagaacaaggccatgtccacgtgcaccactcgtgtcattattat acttcttatgtttggacctgctatcttcatctacatgtgccctttcagggccttaccagctgacaagatggtttctctctttcacacagtgatctt tccattgatgaatcctatgatttatacccttcgcaaccaggaagtgaaaacttccatgaagaggttattgattcgttgtcttgtgctgtgccg attaatgacacagactcacacacggagtgggttaaggaacagaaagtttattaggcaagaaggaagagaagagcttccccatacaga gggagaagca **(SEQ ID NO: 103)**

MOOSE05802 ctg832 2973509..2973633, 2988359..2988723, 2988742..2989221

LEAAHIWISIPFCVVYLLALLGNGSLLFIIKTEPSLHEPMYLFLCMLAVVDLVV CSTAVPKLLSLFWFHDGEIRFETCLSLVFLIHSCSTMESGFFLAMAFDRYVAICNPLRH SAILTRAVIGRVGLAIVLRGIALLSPHSFLLRWLPYCRTHIISHTYCEIACAETKFRRAY SLIVAFLTGVVDFILIIYSYVLILHTVFQLPSKDARLKSLGTCGSHVCVILVSYTPAFFS FLTHRFGHHVAPHFHIFVANIYLLVPPMVNPIIYGVRTKRIWDRFLKVFRLNFQCHIFV ITDHKRLSIISSFPIKEAACC KQRFCMKLCRR **(SEQ ID NO: 106)**

ttggaagctgctcacatctggatctccatccccttttgtgtggtctacctgttggccctactgggaaacggctctcttctgtttatc

atcaagacagagcccagcctccatgagccaatgtacctcttcctatgcatgctggctgtagttgatcttgttgtgtgttctacagctgtgcc
caaacttctcagtctcttctggttccatgatggagagattcgctttgaaacctgcctctcactcgtgttcctgattcactcttgctccaccatg
gaatctggcttcttcctggccatggcttttgaccgatatgtggccatttgcaatccattaagacattcagctattctgacacgcgctgtaatt
gggagagtgggcctagctattgttctcaggggcatagcacttctcagtcctcactctttcctactacgctggcttccctactgcagaaccc
atatcatttctcacacctactgtgagattgcctgtgctgagacaaaattccgcagagcctacagcctcattgttgccttccttactggggtg
gtagactttatattgatcatttattcttatgtcctcatactccacactgtcttccagctcccatccaaagatgcccggctcaaatctttgggcac
ctgtggctcccatgtctgtgtcatcttagtatcctatactccagccttcttctcgtttctcacccacaggtttgggcaccatgtggctccccat
tttcacatatttgtggccaacatctatcttcttgtcccacccatggtgaaccccattatctatggggtaagaaccaaaaggatttgggacag
gttccttaaagttttcaggttaaatttccagtgccacatatttgtaatcactgatcataaaagactcagtataatatcttctttccccataaaaga
agcagcctgctgcaaacaaaggttctgcatgaagttatgcaggcga **(SEQ ID NO: 105)**

MOOSE05811 ctg15944 2627738..2628080, 2633616..2633643, 2638652..2639093, 2664854..2664991

NPEMNVVLSVLFLLIYLITVLGNFWIIIILASAQLHSPMYFFLSQLAFLDFCYSS
VLIPKMLVNYIAGQKVISYHGCLLQYSFVSLFLTTECFLLAAMACDRYLAVCHPLHY
KEHRVQEPIRCSLISVWVISSLAFCDSSINHFFCDTTALLALSCVDTFGTEMVSFVLAG
FTLLSSLLIITVTYIIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPDNTS
SLTQAQVASVFYTIVIPMLNPLIYSLRNKDVKNALLRCSGAVSAHCKLCLLNSRHSPA
SASQVAGTTGARHHARLFFLFLVET **(SEQ ID NO: 108)**

aaccctgaaatgaatgttgtccttctgtgctctttctattaatctatctcattactgtcttgggcaacttttggattatcataataattc
tggctagtgcccaactccattcacccatgtacttttttccttagccagttggctttcttagatttctgctattcttcagtcttgattcctaaaatgtt
ggtgaattacatagcaggacagaaagtcatctcttatcacggttgcctccttcagtattcctttgtcagcttgttcctgactactgaatgcttc
ctcctggctgccatggcatgtgatcggtatctcgctgtttgccacccacttcactacaaagaacatagagtccaggagccaattagatgc
tcgctgatatctgtctgggtgataagcagtttggcgttctgtgattccagcatcaatcatttttttttgtgacaccacagctcttttagcactctc
ctgtgtagatacattcggcacagaaatggtgagctttgtcttagctggattcactcttcttagctctctccttatcatcacagtcacttatatca
tcatcatctcagccatcctgaggatccagtcagcagcaggcaggcagaaggccttctccacctgcgcatcccacctcatggctgtaact
atcttttatgggtctctgattttcacctatttgcaacctgataacacatcatcgctgacccaggcgcaggtggcatctgtattctatacgattg
tcattcccatgctgaatccactcatctacagtctgaggaacaaagatgtgaaaaatgctcttctgagatgcagtggtgccgtctcggctca
ctgcaagctctgcctcctgaattcacgccattctcctgcctcagcctcccaagtcgctgggactacaggcgcccgccaccacgcaagg
ctatttttttttatttttagtagagacg **(SEQ ID NO: 107)**

MOOSE05812 ctg4256 14956033..14956176, 14958553..14958878, 14958906..14959383

QSRIGLFVFTLIFLIFLMALIGNLSMILLIFLDIHLHTPMYFLLSQLSLIDLNYISTI
VPKMVYDFLYGNKSISFTGCGIQSFFFLTLAVAEGLLLTSMAYDRYVAICFPLHYPIRI
SKRVCVMMITGSWMISSINSCAHTVYALCIPYCKSRAINHFFSCTDTWVYESTVFLSS
TIFLVLPFTGIACSYGRVLLAVYRMHSAKGRNKVYSTCSTHLTVVYFYYAPFAYTYV
RARSLRSPTEDKILAVFYTILTPMLNPIIYSLRNKESFCTAKETTIRVNRQPTEWEKIFA
TYSSDKGLISRIYNELKQTYKKKT **(SEQ ID NO: 110)**

caatcaagaattggccttttcgtattcaccctcatttttctcattttcctaatggctctaattggaaatctatccatgattcttctcatct
ttttggacatccatctccacacacctatgtatttcctacttagtcagctctccctcattgacctaaattacatctccaccattgttccaaagatg
gtttatgattttctgtatggaaacaagtctatctccttcactggatgtgggattcagagtttcttcttcttgactttagcagttgcagaagggct
gctcctgacatcaatggcctatgatcgttatgtggccatttgctttcctctccactatcccatccgtataagcaaaagagtgtgtgtgatgat
gataacaggatcttggatgataagctctatcaactcttgtgctcacacagtatatgcactctgtatcccatattgcaagtccagagccatca
atcatttttttctcctgcacagacacttgggtctatgagagcacagtgtttttgagcagcaccatctttcttgtgcttcctttcactggtattgcat
gttcctatggccgggttctccttgctgtctaccgcatgcactctgcaaaagggaggaataaggtctattcaacctgtagcacccacctca
ctgtggtgtacttctactatgcacccttgcttatacctatgtacgtgcaagatccctgcgatctccaaccgaggacaagattctggctgttt
tctacaccatcctcaccccaatgctcaaccccatcatctacagcctgagaaacaaggagagcttctgcacagcaaaagaaactaccat

cagagtgaacaggcaacctacagaatgggagaaaatttttgcaacctactcatctgacaaagggctaatatccagaatctacaatgaac
tcaaacaaacttacaagaaaaaaaca **(SEQ ID NO: 109)**

MOOSE05827 ctg4256 15055783..15055926, 15062025..15062324,
15062361..15062855
PSRIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLIDLNYISTI
VPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLLASMAYDRYIAICFPLHYLIR
MSKRVCVLMITGSWIIGSINACAHTVYVLHIPYCRSRAINHFFCDVPAMGTVFLSATI
FLVFPFIGISCSYGQVLFAVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRP
RSLRSPTEDKVLAVFYTILTPMLNPIIYSLRNKESKRKKRKERKRKRKKRKKERERKR
EREKEKERKERKEREKERKERKKE **(SEQ ID NO: 112)**
ccatcaagaattgacctttttcttcttcattctcattgttttcattttcctgatggctctaattggaaacctgtccatgattcttctcatctt
cttggacacccatctccacacacccatgtatttcctactgagtcagctctccctcattgacctaaattacatctccaccattgttcctaagat
ggcatctgattttctgcatggaaacaagtctatctccttcactgggtgtgggattcagagtttcttcttcttggcattaggaggtgcagaagc
actacttttggcatctatggcctatgatcgttacattgctatttgctttcctctccactatctcatccgcatgagcaaaagagtgtgtgtgctga
tgataacagggtcttggatcataggctcgatcaatgcttgtgctcacactgtatatgtactccatattccttattgccgatccagggccatca
atcatttcttctgtgatgtcccagcaatgggcacagtgtttttgagtgccaccatctttctcgtgtttcccttcattggtatttcatgttcctatgg
ccaggttctctttgctgtctaccacatgaaatctgcagaagggaggaagaaagcctatttgacctgcagcacccacctcactgtagtaac
tttctactatgcaccttttgtctacacttatctacgtccaagatccctgcgatctccaacagaggacaaggttctggctgtcttctacaccatc
ctcaccccaatgctcaaccccatcatctatagcctgaggaacaaggagagcaagagaaagaaaagaaaggaaagaaagagaaaaa
gaaagaaaagaaagaaagaaagagaaagaaagagagaaagagagaaagagaaagaaagaaaagaaaggaaagaaagagaaa
aagaaagaaaagaaagaaagaaagag **(SEQ ID NO: 111)**

MOOSE05861 ctg15944 6729088..6729914, 6731331..6731469
SRELSQVLFTFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLLRNLSILDICF
SSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRYIAISKPLHY
MTIMSRGRCTGLIVGFLGGGLVHSIAQISLLLPLPVCGPNVLDTFYCDVPQVLKLACT
DTFTLELLMISNNGLVSWFVFFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVVTL
HFVPCIYVYARPFTALPTDTAISVTFTVISPLLNPIIYTLRNQEMNNRSRHLSKKKKKR
KDKKKPACAKKENEVRLCHICVTVNSVQPWRNT **(SEQ ID NO: 114)**
tcccgagaactgagccaggtcttatttaccttcctgtttttggtgtacatgacaactctaatgggaaacttcctcatcatggttac
agttacctgtgaatctcaccttcatacgcccatgtacttcctgctccgcaacctgtctattcttgacatctgcttttcctccatcacagctccta
aggtcctgatagatcttctatcagagacaaaaaccatctccttcagtggctgtgtcactcaaatgttcttcttccaccttctgggggggagca
gacgtttttttctctctctgtgatggcgtttgaccgctatatagccatctccaagcccctgcactatatgaccatcatgagtagggggcgatg
cacaggcctcatcgtgggcttcctgggtgggggggcttgtccactccatagcgcagatttctctattgctcccactccctgtctgtggaccc
aatgttcttgacactttctactgcgatgtcccccaggtcctcaaacttgcctgcactgacaccttcactctggagctcctgatgatttcaaat
aatgggttagtcagttggtttgtattcttctttctcctcatatcttacacggtcatcttgatgatgctgaggtctcacactggggaaggcagga
ggaaagccatctccacctgcacctcccacatcaccgtggtgaccctgcatttcgtgccctgcatctatgtctatgcccggcccttcactg
ccctccccacagacactgccatctctgtcaccttcactgtcatctccccttgctcaatcctataatttacacgctgaggaatcaggaaatg
aacaacagatcaagacacttgtcaaaaaaaaaaaagaaaagaaaagacaaaaagaaaccagcatgcgcaaagaaagaaaatgagg
tgagattgtgccacatttgtgtaacagtgaactcagtgcagccatggcgtaataca **(SEQ ID NO: 113)**

MOOSE05863 ctg15907 31055206..31056122, 31068740..31068797
WQQQQVLLFALFLCLYLTGLFGNLLILLAIGSDHCLHTPMYFFLANLSLVDLC
LPSATVPKMLLNIQTQTQTISYPGCLAQMYFCMMFANMDNFLLTVMAYDRYVAICH
PLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMAHLHFCSDNVIHHFFCDINSLLP
LSCSDTSLNQLSVLATVGLIFVVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHL
ALVILFYGAITGVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFIYSLRNNELKGTLKK
TLSRPGAVAHACNPSTLGGRGGNTWTEAKYVHREVHIMIKR **(SEQ ID NO: 116)**

tggcaacaacagcaggtgctactctttgcacttttcctgtgtctctatttaacagggctgtttggaaacttactcatcttgctggc
cattggctcggatcactgccttcacacacccatgtatttcttccttgccaatctgtccttggtagacctctgccttccctcagccacagtccc
caagatgctactgaacatccaaacccaaacccaaaccatctcctatcccggctgcctggctcagatgtatttctgtatgatgtttgccaat
atggacaattttcttctcacagtgatggcatatgaccgttacgtggccatctgtcacccctttacattactccaccattatggccctgcgcctc
tgtgcctctctggtagctgcaccttgggtcattgccattttgaaccctctcttgcacactcttatgatggcccatctgcacttctgctctgata
atgttatccaccatttcttctgtgatatcaactctctcctcccctctgtcctgttccgacaccagtcttaatcagttgagtgttctg
gctacggtggggctgatctttgtggtaccttcagtgtgtatcctggtatcctatatcctcattgtttctgctgtgatgaaagtcccttctgccc
aaggaaaactcaaggctttctctacctgtggatctcaccttgccttggtcattcttttctatggagcaatcacaggggtctatatgagcccct
tatccaatcactctactgaaaaagactcagccgcatcagtcatttttatggttgtagcacctgtgttgaatccattcatttacagtttaagaaa
caatgaactgaaggggactttaaaaaagaccctaagccgaccgggcgcggtggctcacgcctgtaatcccagcactttgggaggcc
gaggcggaaatacatggacagaagcaaaatatgttcatagagaagtacatataatgatcaagaga **(SEQ ID NO: 115)**

MOOSE05908 ctg15944 2316216..2316693, 2331854..2331911, 2333360..2333372, 2338898..2339200, 2350975..2351085

YPEIQVPLFLVFLFVYTVTVVGNLGMIIIIRLNSKLHTIMCFFLSHLSLTDFCFST
VVTPKLLENLVVEYRTISFSGCIMQFCFACIFGVTETFMLAAMAYDRFVAVCKPLLY
TTIMSQKLCALLVAGSYTWGIVCSLILTYFLLDLSFCESTFINNFISFNSTLYYKIYHQT
FSCICEHFLPMCTLLIILTSYVFIFVTVLKIRSVSGRHKAFSTWASHLTSITIFHGTILFLY
CVPNSKNSRQTVKVASVFYTVVNPMLNPLIYSLRNKDVKDAFWKLIHTQSRRRQSL
RRSLRNSHLMTTSIEEGVTHTSTILELCSS **(SEQ ID NO: 118)**

tacccagaaatccaggttccactctttctggttttcttgttcgtctacacagtcactgtagtggggaacttgggcatgataataat
catcagactcaattcaaaactccatacaatcatgtgctttttccttagtcacttgtccttgacagacttctgtttttccactgtagttacacctaa
actgttggagaacttggttgtggaatacagaaccatctctttctctggttgcatcatgcaatttttgttttgcttgcatttttggagtgacagaaa
ctttcatgttagcagcgatggcttatgaccgttttgtggcagtttgtaaacccttgctgtataccactattatgtctcagaagctctgtgctctt
ctggtggctgggtcctatacatgggggatagtgtgctccctgatactcacatattttcttcttgacttatcgttttgtgaatctaccttcataaat
aattttatctctttcaactccaccttatactatataaaatataccaccaaaccttctcctgtatatgtgagcactttctgccaatgtgtacactactg
atcatcctcacttcctatgttttcatttttgtgactgtactaaaaatccgttctgttagtgggcgccacaaagccttctccacctgggcctccc
acctgacttctatcaccatcttccatgggaccatccttttcctttactgtgtacccaactccaaaaactctcggcaaacagtcaaagtggcc
tctgtattttacacagttgtcaaccccatgctgaaccctctgatctacagcctaaggaataaagacgtgaaggatgctttctggaagttaat
acatacacaatcaagaaggaggcagagcttgaggaggtccttgagaaattcccatttaatgaccaccagcattgaagaaggagtcacc
cacaccagtaccattctggagctctgctcatcc **(SEQ ID NO: 117)**

MOOSE05917 ctg30162 1982852..1982944, 1985177..1985529, 1985575..1986055

PLRLRTLFFVFFFLIYILTQLGNLLILITVWADPRLHARPMYIFLGVLSVIDMSIS
SIIVPRLMMNFTLGVKPIPFGGCVAQLYFYHFLGSTQCFLYTLMAYDRYLAICQPLRY
PVLMTAKLSALLVAGAWMAGSIHGALQAILTFRLPYCGPNQVDYFFFNELVTFVDIG
VVVASCFSLILLSYIQIIQAILRIHTADGRRRAFSTCGAHVTVVTVYYVPCAFIYLRPET
NSPLDGAAALVPTAITPFLNPLIYTLRNQEVKLALKRMLRSPRTPSEHFGRPRRVDHL
RSGVRDQPNQHGETASLPKI **(SEQ ID NO: 120)**

ccactcaggctaaggacactctttttgtgttctttttctaatctacatcctgactcagctgggaaacctgcttattttaatcactgt
ctgggcagacccaaggctccatgcccgccccatgtacatctttcttggtgttctctcagtcattgatatgagcatctcctccatcattgtccc
tcgcctcatgatgaacttcactttaggtgtcaaacccatcccatttggtggctgtgttgctcaactctatttctatcacttcctgggcagcacc
cagtgcttcctctacaccctaatggcctatgacaggtacctggcaatatgtcagcccctgcgctaccctgtgctcatgactgctaagctg
agcgccttgcttgtggctggagcctggatggcaggatccatccatggggctctccaggccatcctaaccttccgcctgccctactgtgg
gcccaatcaggtggattacttcttcttcaacgagctggtgacgtttgtagacattggggtggtggttgccagttgcttctccctgatcctcct
ctcctacatacagatcattcaggccatcctgagaatccacacagctgatgggcggcgccgggcttttcaacttgtggagcccatgtaa
ccgtggtcaccgtgtactatgtgccctgtgccttcatctacctgaggcctgaaaccaacagccccctggatggggcagctgccctagtc
cccacggccatcactcctttcctcaaccccccttatctacactctgcggaaccaagaggtgaagctggccctgaaaagaatgctcagaa

gcccaagaactccgagtgagcactttgggaggccaaggcgggtggatcacctgaggtcgggagttcgagaccagcctaaccaacat ggagaaactgcatctttaccaaaaata **(SEQ ID NO: 119)**

MOOSE06051 ctg15064 38069881..38070569, 38071866..38071965, 38089519..38089577, 38100385..38100508

DPIVTPHLISLYFIVLIGGLVGVISILFLLVKMNTRSVTTMAVINLVVVHSVFLL TVPFRLTYLIKKTWMFGLPFCKFVSAMLHIHMYLTFLFYVVILVTRYLIFFKCKDKVE FYRKLHAVAASAGMWTLVIVIVVPLVVSRYGIHEEYNEEHCFKFHKELAYTYVKIIN YMIVIFVIAVAVILLVFQVFIIMLMVQKLRHSLLSHQEFWAQLKNLFFIGVILVCFLPY QPHCVMFPSLCPCVFIVQLPLLSENMRCLVFCSCLIHFLLYIFIVHNMRYSYMYNFVS CPLPACNAVMQCSGSNLEQSRKQYSQCSRPGTARGKL **(SEQ ID NO: 122)**

gatcctatagtgacaccccacttaatcagcctctacttcatagtgcttattggcgggctggtgggtgtcatttccattcttttcctc ctggtgaaaatgaacacccggtcagtgaccaccatggcggtcattaacttggtggtggtccacagcgtttttctgctgacagtgccatttc gcttgacctacctcatcaagaagacttggatgtttgggctgcccttctgcaaatttgtgagtgccatgctgcacatccacatgtacctcac gttcctattctatgtggtgatcctggtcaccagatacctcatcttcttcaagtgcaaagacaaagtggaattctacagaaaactgcatgctg tggctgccagtgctggcatgtggacgctggtgattgtcattgtggtacccctggttgtctcccggtatggaatccatgaggaatacaatg aggagcactgttttaaatttcacaaagagcttgcttacacatatgtgaaaatcatcaactatatgatagtcatttttgtcatagccgttgctgt gattctgttggtcttccaggtcttcatcattatgttgatggtgcagaagctacgccactctttactatcccaccaggagttctgggctcagct gaaaaacctatttttttataggggtcatccttgtttgtttccttccctaccagccccattgtgtgatgttcccctccctgtgtccatgtgttttcatt gttcaactcccacttctaagtgagaacatgcggtgtttggttttctgttcctgtttgattcatttttattgtatatatttatagtgcacaacatgag gtattcatacatgtataacttcgtcagctgtcctttgccagcatgtaatgcagtgatgcaatgctctggtagtaatttggaacaatccaggaa gcaatattctcagtgttcaaggcccggcactgcccgggggaaatta **(SEQ ID NO: 121)**

MOOSE07369 ctg15361 27381078..27381945, 27422885..27422949

HVLNFQELFFLVFGVSTLIVVFLMVLIILTTLVGNLIVIVSISHFKQLHTPTNWLI HSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCKIHTSTDIMLSSASIFHLSFISID RYYAVCDPLRYKAKMNILVICVMIFISWSVPAVFAFGMIFLELNFKGAEEIYYKHVH CRGGCSVFFSKISGVLTFMTSFYIPGSIMLCVYYRIYLIAKEQARLISDANQKLQIGLE MKNGISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGY LNSTFNPMVYAFFYPWFRKALKM **(SEQ ID NO: 124)**

catgttcttaatttccaagaactctttttcttgtcttcggagtttcaacacttattgttgttttttaatggtgctcataattctgaccac actcgttggcaatctgatagttattgtttctatatcacacttcaaacaacttcataccccaacaaattggctcattcattccatggccactgtg gactttcttctggggtgtctggtcatgccttacagtatggtgagatctgctgagcactgttggtattttggagaagtcttctgtaaaattcaca caagcaccgacattatgctgagctcagcctccatttccatttgtctttcatctccattgaccgctactatgctgtgtgtgatccactgagata taaagccaagatgaatatcttggttatttgtgtgatgatcttcattagttggagtgtccctgctgtttttgcatttggaatgatctttctggagct aaacttcaaaggcgctgaagagatatattacaaacatgttcactgcagaggaggttgctctgtcttctttagcaaaatatctggggtactg acctttatgacttctttttatatacctggatctattatgttatgtgtctattacagaatatatcttatcgctaaagaacaggcaagattaattagtg atgccaatcagaagctccaaattggattggaaatgaaaaatggaatttcacaaagcaaagaaaggaaagctgtgaagacattggggat tgtgatgggagttttcctaatatgctggtgcccttttctttatctgtacagtcatggacccttttcttcactacattattccacctactttgaatgat gtattgatttggtttggctacttgaactctacatttaatccaatggtttatgcatttttctatccttggtttagaaaagcactgaagatg **(SEQ ID NO: 123)**

Table III

ctg14797_MOOSE00162.xml	Angiotensin
ctg16465_MOOSE00638.xml	Class A Orphan
ctg16008_MOOSE00693.xml	Class A Orphan
ctg16282_MOOSE00717.xml	Class A Orphan
ctg16228_MOOSE00721.xml	Class A Orphan
ctg877_MOOSE00741.xml	Class A Orphan
ctg15378_MOOSE00766.xml	Class A Orphan
ctg78_MOOSE00772.xml	Class A Orphan
ctg15540_MOOSE00775.xml	Class A Orphan
ctg16537_MOOSE00779.xml	Class A Orphan
ctg30162_MOOSE00804.xml	Class A Orphan
ctg15378_MOOSE00814.xml	Class A Orphan
ctg15907_MOOSE00818.xml	Class A Orphan
ctg14294_MOOSE00822.xml	Class A Orphan
ctg15968_MOOSE00826.xml	Class A Orphan
ctg14145_MOOSE00829.xml	Class A Orphan
ctg14667_MOOSE00838.xml	Class A Orphan
ctg14333_MOOSE00841.xml	Class A Orphan
ctg15064_MOOSE00843.xml	Class A Orphan
ctg15944_MOOSE00846.xml	Class A Orphan
ctg14333_MOOSE00855.xml	Class A Orphan
ctg16279_MOOSE00861.xml	Class A Orphan
ctg18147_MOOSE00872.xml	Class A Orphan
ctg15944_MOOSE00880.xml	Class A Orphan
ctg15944_MOOSE00882.xml	Class A Orphan
ctg15296_MOOSE00886.xml	Class A Orphan
ctg17659_MOOSE00899.xml	Class A Orphan
ctg18867_MOOSE00930.xml	Class A Orphan
ctg3235_MOOSE00941.xml	Class A Orphan
ctg15907_MOOSE00981.xml	Class A Orphan
ctg17802_MOOSE00994.xml	Class A Orphan
ctg12634_MOOSE01139.xml	Class B Secretin Receptor
ctg15998_MOOSE01146.xml	Class B Secretin Receptor
ctg12559_MOOSE01148.xml	Class B Secretin Receptor
ctg15361_MOOSE01165.xml	Class C Metabotropic Glutamate Receptor
ctg14779_MOOSE01172.xml	Class C Metabotropic Glutamate Receptor
ctg17658_MOOSE01176.xml	Class C Metabotropic Glutamate Receptor
ctg13655_MOOSE01371.xml	Frizzled related GPCR
ctg17341_MOOSE01451.xml	Gonadotropin receptor
ctg37_MOOSE01609.xml	Lysosphingolipid Receptor
ctg15037_MOOSE02359.xml	Mollusc Rhodopsine-like GPCR
ctg15907_MOOSE02360.xml	Mollusc Rhodopsine-like GPCR
ctg12376_MOOSE02352.xml	unclassified GPCRs
ctg13067_MOOSE01169.xml	Class C Metabotropic glutamate pheromone
ctg13284_MOOSE00810.xml	Class A Orphan other
ctg14473_MOOSE01192.xml	Class Y G proteins

ctg15361_MOOSE05621.xml	Class A Orphan GPCRs
ctg3235_MOOSE05712.xml	Class A Orphan GPCRs
ctg3235_MOOSE05732.xml	Class A Orphan GPCRs
ctg3235_MOOSE05740.xml	Class A Orphan GPCRs
ctg4256_MOOSE05748.xml	Class A Orphan GPCRs
ctg30162_MOOSE05757.xml	Class A Orphan GPCRs
ctg13495_MOOSE05798.xml	Class A Orphan GPCRs
ctg832_MOOSE05802.xml	Class A Orphan GPCRs
ctg15944_MOOSE05811.xml	Class A Orphan GPCRs
ctg4256_MOOSE05812.xml	Class A Orphan GPCRs
ctg4256_MOOSE05827.xml	Class A Orphan GPCRs
ctg15944_MOOSE05861.xml	Class A Orphan GPCRs
ctg15907_MOOSE05863.xml	Class A Orphan GPCRs
ctg15944_MOOSE05908.xml	Class A Orphan GPCRs
ctg30162_MOOSE05917.xml	Class A Orphan GPCRs
ctg15064_MOOSE06051.xml	Class A Orphan GPCRs
ctg15361_MOOSE07369.xml	Serotonin Gated Ion Channel Receptor

Table IV

OTHER GPCRs

##########

RA (Rheumatoid Arthritis)

Locus2	Marker:D6S265	Lod:3	CM RANGE of one LOD drop: 6
	MOOSE05863	Class A Orphan other DISTANCE: -1.97 Mb	
	MOOSE06011	Class A Orphan other DISTANCE: 8.000 Mb	

##########

COPD (Chronic Obstructive Pulmonary Disease)

Locus4	Marker:D19S884	Lod:2.9	CM RANGE of one LOD drop: 20
	MOOSE05784	Class A Orphan other DISTANCE: 0.959 Mb	

##########

Asthma

Locus1	Marker:D3S3698	Lod:3.8	CM RANGE of one LOD drop: 15
	MOOSE06049	Class A Orphan other	

DISTANCE: -12.8 Mb

##########

NIDDM (Non-insulin dep. Diabetes)

Locus4	Marker:D17S785	Lod:3.2	CM RANGE of one LOD drop: 10
	MOOSE05814	Class A Orphan other DISTANCE: -2.47 Mb	

##########

Obesity

Locus4	Marker:D14S283	Lod:3.2	CM RANGE of one LOD drop: 12
	MOOSE05757	Class A Orphan other DISTANCE: -2.15 Mb	
	MOOSE05917	Class A Orphan other DISTANCE: -0.65 Mb	
Locus5	Marker:SHGC-1089	Lod:4.6	CM RANGE of one LOD drop: 20
	MOOSE05798	Class A Orphan other DISTANCE: -9.98 Mb	

##########

Bipolar (Genomewide scan only)

Locus1	Marker:D1S434	Lod:3.3	CM RANGE of one LOD drop: 5
	MOOSE06105	Class C Metabotropic glutamate pheromone DISTANCE: -10.6 Mb	
	MOOSE06101	Class C Metabotropic glutamate pheromone DISTANCE: -6.55 Mb	
Locus3	Marker:D16S3041	Lod:2.5	CM RANGE of one LOD drop:25
	MOOSE05745	Class A Orphan other DISTANCE: 0.725 Mb	

##########

OP (Osteoporosis)

Locus5	Marker:D20S194	Lod:5.05	CM RANGE of one LOD drop: 5
	MOOSE05705	Class A Orphan other DISTANCE: -0.86 Mb	

##########

Alzheimer's Disease

Locus1	Marker:D13S785	Lod:4.06	CM RANGE of one LOD drop: 7
	MOOSE05635	Class A Orphan other DISTANCE: 4.447 Mb	

##########

AMD (Age-related Macular Degeneration)

Locus2	Marker:D3S3631	Lod:2.91	CM RANGE of one LOD drop:20
	MOOSE06049	Class A Orphan other DISTANCE: -10.5 Mb	

##########

MI (Myocardial Infarction)

Locus1	Marker:D6S282	Lod:1.99	CM RANGE of one LOD drop:19
	MOOSE06011	Class A Orphan other DISTANCE: -7.07 Mb	
	MOOSE07334	Rhodopsin Other DISTANCE: 5.065 Mb	
Locus5	Marker:D13S167	Lod:2.38	CM RANGE of one LOD drop:25
	MOOSE05635	Class A Orphan other DISTANCE: 2.102 Mb	

##########

Schizophrenia

Locus1	Marker:D3S1315	Lod:2.73	CM RANGE of one LOD drop:21
	MOOSE06103	Class C Metabotropic glutamate pheromone DISTANCE: 5.243 Mb	

##########

Osteoarthritis

Locus3	Marker:D16S401	Lod:2.7	CM RANGE of one LOD drop: 6
	MOOSE05745	Class A Orphan other DISTANCE: -4.43 Mb	

##########

Longevity

Locus1	Marker:D9S1826	Lod:2.30	CM RANGE of one LOD drop:15
	MOOSE06089	Class B Secretin like DISTANCE: -12.5 Mb	
Locus2	Marker:D11S987	Lod:2.07	CM RANGE of one LOD drop:12
	MOOSE05934	Class A Orphan other DISTANCE: -14.1 Mb	
	MOOSE05861	Class A Orphan other DISTANCE: -12.4 Mb	
	MOOSE05761	Class A Orphan other DISTANCE: -0.76 Mb	
	MOOSE05781	Class A Orphan other DISTANCE: 0.884 Mb	
	MOOSE05938	Class A Orphan other DISTANCE: 1.364 Mb	

##########

Psoriasis

Locus1	Marker:GDB:182383	Lod:10.61	CM RANGE of one LOD drop: 2
	MOOSE05863	Class A Orphan other DISTANCE: -3.49 Mb	
	MOOSE06011	Class A Orphan other DISTANCE: 6.481 Mb	
Locus2	Marker:D7S669	Lod:1.81	CM RANGE of one LOD drop:20
	MOOSE06127	Class Y G proteins DISTANCE: 2.208 Mb	

CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule comprising a G protein-coupled receptor (GPCR) gene, wherein the GPCR gene has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.

2. A nucleic acid encoding a polypeptide, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

3. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.

4. An isolated nucleic molecule that hybridizes under high stringency conditions to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

5. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, and hybridizes to the first nucleic acid under high stringency conditions.

6. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
   (a) the nucleic acid sequences as shown in Tables I and II;
   (b) the complement of one of the nucleic acid sequences are shown in Tables I and II; or
   (c) a nucleic acid encoding an amino acid molecule as shown in Tables I and II;

wherein the nucleic acid molecule is operably linked to a regulatory sequence.

7. A recombinant host cell comprising the vector of Claim 6.

8. A method for producing a polypeptide encoded by an isolated nucleic acid molecule, comprising culturing the recombinant host cell of Claim 7 under conditions suitable for expression of the nucleic acid molecule.

9. An isolated polypeptide encoded by the nucleotide sequence of the group of nucleic acid sequences as shown in Tables I and II, or the complements thereof.

10. The isolated polypeptide of Claim 9, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

11. An isolated polypeptide comprising an amino acid sequence, wherein the amino acid sequence is greater than about 95% identical to an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

12. A fusion protein comprising an isolated polypeptide of Claim 2.

13. A fusion protein comprising an isolated polypeptide of Claim 11.

14. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 2, or to a fragment or variant of said amino acid sequence.

15. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 11, or to a fragment or variant of said amino acid sequence.

16. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 1 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.

17. A method of identifying an agent which alters the activity of a GPCR, the method comprising:

(a) contacting a polypeptide of Claim 9, or a derivative or fragment thereof, with an agent to be tested;

(b) assessing the level of activity of the polypeptide or derivative or fragment thereof; and

(c) comparing the level of activity with a level of activity of the polypeptide or active derivative or fragment thereof in the absence of the agent;

wherein if the level of activity of the polypeptide or derivative or fragment thereof in the presence of the agent differs, by an amount that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters activity of a GPCR.

18. An agent that alters the activity of a GPCR, identifiable according to the method of Claim 17.

19. The agent of Claim 18, where the agent is selected from the group consisting of: a GPCR gene binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

20. A method of altering activity of a polypeptide encoded by a GPCR gene, comprising contacting the polypeptide with an agent of Claim 19.

21. A method of identifying an agent which alters interaction of the polypeptide of Claim 9 with a GPCR gene binding agent, comprising:

a) contacting the polypeptide or a derivative or fragment thereof, and the binding agent, with an agent to be tested;

b) assessing the interaction of the polypeptide or derivative or fragment thereof with the binding agent; and

c) comparing the level of interaction with a level of interaction of the polypeptide or derivative or fragment thereof with the binding agent in the absence of the agent,

wherein if the level of interaction of the polypeptide or derivative or fragment thereof in the presence of the agent differs by an amount that is statistically significant, from the level of interaction in the absence of the

agent, then the agent is an agent that alters interaction of the polypeptide with the binding agent.

22. An agent that alters interaction of a GPCR polypeptide with a GPCR binding agent, identifiable according to the method of Claim 21.

23. An agent that alters interaction of a GPCR polypeptide with a GPCR binding agent, selected from the group consisting of: a second GPCR binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

24. A method of altering interaction of a GPCR polypeptide with a GPCR binding agent, comprising contacting the GPCR gene polypeptide and/or the GPCR gene binding agent with an agent of Claim 23.

25. A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:

a) contacting a solution containing a nucleic acid comprising the promoter region of the GPCR gene operably linked to a reporter gene with an agent to be tested;

b) assessing the level of expression of the reporter gene; and

c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent,

wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.

26. An agent that alters expression of the GPCR gene, identifiable according to the method of Claim 25.

27. A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:

a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;

b) assessing expression of the nucleic acid, derivative or fragment; and

c) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent,

wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.

28. The method of Claim 27, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.

29. An agent that alters expression of a GPCR gene, identifiable according to the method of Claim 27.

30. An agent that alters expression of a GPCR gene, selected from the group consisting of: antisense nucleic acid to a GPCR gene; a GPCR gene polypeptide; a GPCR gene receptor; a GPCR gene binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme.

31. A method of altering expression of a GPCR gene, comprising contacting a cell containing a GPCR gene with an agent of Claim 30.

32. A method of identifying a polypeptide which interacts with a GPCR gene polypeptide, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a GPCR gene polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a GPCR polypeptide.

33. A GPCR gene therapeutic agent selected from the group consisting of: a GPCR gene or fragment or derivative thereof; a polypeptide encoded by a GPCR gene; a G-protein; a GPCR gene binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters GPCR gene expression; an agent that alters activity of a polypeptide encoded by a GPCR gene; an agent that alters posttranscriptional processing of a polypeptide

encoded by a GPCR gene; an agent that alters interaction of a GPCR gene with a GPCR gene binding agent; an agent that alters transcription of splicing variants encoded by a GPCR gene; and a ribozyme.

34. A pharmaceutical composition comprising a GPCR gene therapeutic agent of Claim 33.

35. The pharmaceutical composition of Claim 34, wherein the GPCR gene therapeutic agent is an isolated nucleic acid molecule comprising a GPCR gene or fragment or derivative thereof.

36. The pharmaceutical composition of Claim 34, wherein the GPCR gene therapeutic agent is a polypeptide encoded by the GPCR gene.

37. A method of treating a disease or condition associated with a GPCR in an individual, comprising administering a GPCR gene therapeutic agent to the individual, in a therapeutically effective amount.

38. The method of Claim 37, wherein the GPCR gene therapeutic agent is a GPCR gene agonist.

39. The method of Claim 38 wherein the GPCR gene therapeutic agent is a GPCR gene antagonist.

40. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous GPCR gene and a nucleic acid encoding a GPCR gene polypeptide.

41. A method for assaying a sample for the presence of a GPCR gene nucleic acid, comprising:

a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid under conditions appropriate for hybridization, and

b) assessing whether hybridization has occurred between a GPCR gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid;

wherein if hybridization has occurred, a GPCR gene is present in the nucleic acid.

42. The method of Claim 41, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said GPCR gene nucleic acid.

43. The method of Claim 41, comprising amplification of at least part of said GPCR gene nucleic acid.

44. The method of Claim 41, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid.

45. A reagent for assaying a sample for the presence of a GPCR gene nucleic acid, said reagent comprising a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

46. The reagent of Claim 45, wherein the nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

47. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising in separate containers:

a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid, and

b) reagents for detection of said label.

48. The reagent kit of Claim 47, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

49. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid, and which is capable of acting as a primer for said GPCR gene nucleic acid when maintained under conditions for primer extension.

50. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid, for assaying a sample for the presence of a GPCR gene nucleic acid.

51. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;

b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

c) capable of selectively hybridizing to said GPCR gene nucleic acid;

for assaying a sample for the presence of a GPCR gene nucleic acid that has at least one nucleotide difference from the first nucleic acid.

52. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;

b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

c) capable of selectively hybridizing to said GPCR gene nucleic acid;

for diagnosing a susceptibility to a disease or condition associated with a GPCR.

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Sigurdsson, Gunnar Thor

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Ser Asp Glu Leu Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala
                165                 170                 175

act act ttc tgc ctc ccc ttg gtg ata gtg aca ctt tgc tat acc acg   576
Thr Thr Phe Cys Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr
            180                 185                 190

att atc cac act ctg acc cat gga ctg caa act gac agc tgc ctt aag   624
Ile Ile His Thr Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys
        195                 200                 205

cag aaa gca cga agg cta acc att ctg cta ctc ctt gca ttt tac gta   672
Gln Lys Ala Arg Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val
    210                 215                 220

tgt ttt tta ccc ttc cat atc ttg agg gtc att cgg atc gaa tct cgc   720
Cys Phe Leu Pro Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg
225                 230                 235                 240

ctg ctt tca atc agt tgt tcc att gag aat cag atc cat gaa gct tac   768
Leu Leu Ser Ile Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr
                245                 250                 255

atc gtt tct aga cca tta gct gct ctg aac acc ttt ggt aac ctg tta   816
Ile Val Ser Arg Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu
            260                 265                 270

cta tat gtg gtg gtc agc gac aac ttt cag cag gct gtc tgc tca aca   864
Leu Tyr Val Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr
        275                 280                 285

gtg aga tgc aaa gta agc ggg aac ctt gag caa gca aag aaa att atg   912
Val Arg Cys Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Met
    290                 295                 300

gta tca tct tca tca tca tca cat tat cat cat cat cat cat cat cat   960
Val Ser Ser Ser Ser Ser Ser His Tyr His His His His His His His
305                 310                 315                 320

cac cat tta cat cca gac agc cag aaa ata                           990
His His Leu His Pro Asp Ser Gln Lys Ile
                325                 330
```

<210> 6
<211> 330
<212> PRT
<213> Homo sapiens

<400> 6

```
Ile Pro Leu Lys Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe
 1               5                  10                  15
Leu Val Gly Phe Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe
            20                  25                  30
Lys Met Arg Pro Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala
        35                  40                  45

Cys Thr Asp Leu Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr
    50                  55                  60
Tyr Ala Ser Gly Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe
65                  70                  75                  80
Ile Arg Phe Ser Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu
```

```
                85                  90                  95
Thr Cys Phe Ser Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser
            100                 105                 110
Cys Phe Ser Ile His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val
        115                 120                 125
Val Trp Ile Ile Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile
    130                 135                 140
Thr Ser Thr Asn Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser
145                 150                 155                 160
Ser Asp Glu Leu Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala
                165                 170                 175
Thr Thr Phe Cys Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr
            180                 185                 190
Ile Ile His Thr Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys
        195                 200                 205
Gln Lys Ala Arg Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val
    210                 215                 220
Cys Phe Leu Pro Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg
225                 230                 235                 240
Leu Leu Ser Ile Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr
                245                 250                 255
Ile Val Ser Arg Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu
            260                 265                 270
Leu Tyr Val Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr
        275                 280                 285
Val Arg Cys Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Met
    290                 295                 300
Val Ser Ser Ser Ser Ser Ser His Tyr His His His His His His His
305                 310                 315                 320
His His Leu His Pro Asp Ser Gln Lys Ile
                325                 330
```

<210> 7
<211> 990
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(990)

<400> 7

```
ttc cta gcc ctg agg ctc atg gtt gcc ctg gcc tat ggg ctt gtg ggg   48
Phe Leu Ala Leu Arg Leu Met Val Ala Leu Ala Tyr Gly Leu Val Gly
 1               5                  10                  15

gcc att ggc ttg ctg gga aat ttg gcg gtg ctg tgg gta ctg agt aac   96
Ala Ile Gly Leu Leu Gly Asn Leu Ala Val Leu Trp Val Leu Ser Asn
            20                  25                  30

tgt gcc cgg aga gcc cct ggc cca cct tca gac acc ttc gtc ttc aac   144
Cys Ala Arg Arg Ala Pro Gly Pro Pro Ser Asp Thr Phe Val Phe Asn
        35                  40                  45

ctg gct ctg gcg gac ctg gga ctg gca ctc act ctc ccc ttt tgg gca   192
Leu Ala Leu Ala Asp Leu Gly Leu Ala Leu Thr Leu Pro Phe Trp Ala
    50                  55                  60

gcc gag tcg gca ctg gac ttt cac tgg ccc ttc gga ggt gcc ctc tgc   240
Ala Glu Ser Ala Leu Asp Phe His Trp Pro Phe Gly Gly Ala Leu Cys
```

```
 65                  70                  75                  80

aag atg gtt ctg acg gcc act gtc ctc aac gtc tat gcc agc atc ttc   288
Lys Met Val Leu Thr Ala Thr Val Leu Asn Val Tyr Ala Ser Ile Phe
                 85                  90                  95

ctc atc aca gcg ctg agc gtt gct cgc tac tgg gtg gtg gcc atg gct   336
Leu Ile Thr Ala Leu Ser Val Ala Arg Tyr Trp Val Val Ala Met Ala
            100                 105                 110

gcg ggg cca ggc acc cac ctc tca ctc ttc tgg gcc cga ata gcc acc   384
Ala Gly Pro Gly Thr His Leu Ser Leu Phe Trp Ala Arg Ile Ala Thr
        115                 120                 125

ctg gca gtg tgg gcg gcg gct gcc ctg gtg acg gtg ccc aca gct gtc   432
Leu Ala Val Trp Ala Ala Ala Ala Leu Val Thr Val Pro Thr Ala Val
    130                 135                 140

ttc ggg gtg gag ggt gag gtg tgt ggt gtg cgc ctt tgc ctg ctg cgt   480
Phe Gly Val Glu Gly Glu Val Cys Gly Val Arg Leu Cys Leu Leu Arg
145                 150                 155                 160

ttc ccc agc agg tac tgg ctg ggg gcc tac cag ctg cag agg gtg gtg   528
Phe Pro Ser Arg Tyr Trp Leu Gly Ala Tyr Gln Leu Gln Arg Val Val
                165                 170                 175

ctg gct ttc atg gtg ccc ttg ggc gtc atc acc acc agc tac ctg ctg   576
Leu Ala Phe Met Val Pro Leu Gly Val Ile Thr Thr Ser Tyr Leu Leu
            180                 185                 190

ctg ctg gcc ttc ctg cag cgg cgg caa cgg cgg cgg cag gac agc agg   624
Leu Leu Ala Phe Leu Gln Arg Arg Gln Arg Arg Arg Gln Asp Ser Arg
        195                 200                 205

gtc gtg gcc cgc tct gtc cgc atc ctg gtg gct tcc ttc ttc ctc tgc   672
Val Val Ala Arg Ser Val Arg Ile Leu Val Ala Ser Phe Phe Leu Cys
    210                 215                 220

tgg ttt ccc aac cat gtg gtc act ctc tgg ggt gtc ctg gtg aag ttt   720
Trp Phe Pro Asn His Val Val Thr Leu Trp Gly Val Leu Val Lys Phe
225                 230                 235                 240

gac ctg gtg ccc tgg aac agt act ttc tat act atc cag acg tat gtc   768
Asp Leu Val Pro Trp Asn Ser Thr Phe Tyr Thr Ile Gln Thr Tyr Val
                245                 250                 255

ttc cct gtc act act tgc ttg gca cac agc aat agc tgc ctc aac cct   816
Phe Pro Val Thr Thr Cys Leu Ala His Ser Asn Ser Cys Leu Asn Pro
            260                 265                 270

gtg ctg tac tgt ctc ctg agg cgg gag ccc cgg cag gct ctg gca ggc   864
Val Leu Tyr Cys Leu Leu Arg Arg Glu Pro Arg Gln Ala Leu Ala Gly
        275                 280                 285


acc ttc agg gat ctg cgg gcg gcc agc tgc ctt cga gcc tct tcg gcc   912
Thr Phe Arg Asp Leu Arg Ala Ala Ser Cys Leu Arg Ala Ser Ser Ala
    290                 295                 300

tca cgc tcc agc agt gcc cgg gcc tgc tca ctc tcc cgg agc cgg gcc   960
Ser Arg Ser Ser Ser Ala Arg Ala Cys Ser Leu Ser Arg Ser Arg Ala
305                 310                 315                 320
```

```
tcc agg ctg cca gct tcg gtt gcc cgt tct                          990
Ser Arg Leu Pro Ala Ser Val Ala Arg Ser
                325                 330


<210> 8
<211> 330
<212> PRT
<213> Homo sapiens

<400> 8
Phe Leu Ala Leu Arg Leu Met Val Ala Leu Ala Tyr Gly Leu Val Gly
 1               5                  10                  15
Ala Ile Gly Leu Leu Gly Asn Leu Ala Val Leu Trp Val Leu Ser Asn
            20                  25                  30
Cys Ala Arg Arg Ala Pro Gly Pro Pro Ser Asp Thr Phe Val Phe Asn
        35                  40                  45
Leu Ala Leu Ala Asp Leu Gly Leu Ala Leu Thr Leu Pro Phe Trp Ala
    50                  55                  60
Ala Glu Ser Ala Leu Asp Phe His Trp Pro Phe Gly Gly Ala Leu Cys
65                  70                  75                  80
Lys Met Val Leu Thr Ala Thr Val Leu Asn Val Tyr Ala Ser Ile Phe
                85                  90                  95
Leu Ile Thr Ala Leu Ser Val Ala Arg Tyr Trp Val Val Ala Met Ala
            100                 105                 110
Ala Gly Pro Gly Thr His Leu Ser Leu Phe Trp Ala Arg Ile Ala Thr
        115                 120                 125
Leu Ala Val Trp Ala Ala Ala Ala Leu Val Thr Val Pro Thr Ala Val
    130                 135                 140
Phe Gly Val Glu Gly Glu Val Cys Gly Val Arg Leu Cys Leu Leu Arg
145                 150                 155                 160
Phe Pro Ser Arg Tyr Trp Leu Gly Ala Tyr Gln Leu Gln Arg Val Val
                165                 170                 175
Leu Ala Phe Met Val Pro Leu Gly Val Ile Thr Thr Ser Tyr Leu Leu
            180                 185                 190
Leu Leu Ala Phe Leu Gln Arg Arg Gln Arg Arg Arg Gln Asp Ser Arg
        195                 200                 205
Val Val Ala Arg Ser Val Arg Ile Leu Val Ala Ser Phe Phe Leu Cys
    210                 215                 220
Trp Phe Pro Asn His Val Val Thr Leu Trp Gly Val Leu Val Lys Phe
225                 230                 235                 240
Asp Leu Val Pro Trp Asn Ser Thr Phe Tyr Thr Ile Gln Thr Tyr Val
                245                 250                 255
Phe Pro Val Thr Thr Cys Leu Ala His Ser Asn Ser Cys Leu Asn Pro
            260                 265                 270
Val Leu Tyr Cys Leu Leu Arg Arg Glu Pro Arg Gln Ala Leu Ala Gly
        275                 280                 285
Thr Phe Arg Asp Leu Arg Ala Ala Ser Cys Leu Arg Ala Ser Ser Ala
    290                 295                 300
Ser Arg Ser Ser Ser Ala Arg Ala Cys Ser Leu Ser Arg Ser Arg Ala
305                 310                 315                 320
Ser Arg Leu Pro Ala Ser Val Ala Arg Ser
                325                 330


<210> 9
<211> 969
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
```

<222> (1)...(969)

<400> 9

```
cgg gcc gtg gac gcc tgg ctc gtg ccg ctc ttc ttc gcg gcg ctg atg   48
Arg Ala Val Asp Ala Trp Leu Val Pro Leu Phe Phe Ala Ala Leu Met
 1               5                  10                  15

ctg ctg ggc ctg gtg ggg aac tcg ctg gtc atc tac gtc atc tgc cgc   96
Leu Leu Gly Leu Val Gly Asn Ser Leu Val Ile Tyr Val Ile Cys Arg
            20                  25                  30

cac aag ccg atg cgg acc gtg acc aac ttc tac atc gcc aac ctg gcg   144
His Lys Pro Met Arg Thr Val Thr Asn Phe Tyr Ile Ala Asn Leu Ala
        35                  40                  45

gcc acg gac gtg acc ttc ctc ctg tgc tgc gtc ccc ttc acg gcc ctg   192
Ala Thr Asp Val Thr Phe Leu Leu Cys Cys Val Pro Phe Thr Ala Leu
    50                  55                  60

ctg tac ccg ctg ccc ggc tgg gtg ctg ggc gac ttc atg tgc aag ttc   240
Leu Tyr Pro Leu Pro Gly Trp Val Leu Gly Asp Phe Met Cys Lys Phe
65                  70                  75                  80

gtc aac tac atc cag cag gtc tcg gtg cag gcc acg tgt gcc act ctg   288
Val Asn Tyr Ile Gln Gln Val Ser Val Gln Ala Thr Cys Ala Thr Leu
                85                  90                  95

acc gcc atg agt gtg gac cgc tgg tac gtg acg gtg ttc ccg ttg cgc   336
Thr Ala Met Ser Val Asp Arg Trp Tyr Val Thr Val Phe Pro Leu Arg
            100                 105                 110

gcc ctg cac cgc cgc acg ccc cgc ctg gcg ctg gct gtc agc ctc agc   384
Ala Leu His Arg Arg Thr Pro Arg Leu Ala Leu Ala Val Ser Leu Ser
        115                 120                 125

atc tgg gta ggc tct gcg gcg gtg tct gcg ccg gtg ctc gcc ctg cac   432
Ile Trp Val Gly Ser Ala Ala Val Ser Ala Pro Val Leu Ala Leu His
    130                 135                 140

cgc ctg tca ccc ggg ccg cgc gcc tac tgc agt gag gcc ttc ccc agc   480
Arg Leu Ser Pro Gly Pro Arg Ala Tyr Cys Ser Glu Ala Phe Pro Ser
145                 150                 155                 160

cgc gcc ctg gag cgc gcc ttc gca ctg tac aac ctg ctg gcg ctg tac   528
Arg Ala Leu Glu Arg Ala Phe Ala Leu Tyr Asn Leu Leu Ala Leu Tyr
                165                 170                 175

ctg ctg ccg ctg ctc gcc acc tgc gcc tgc tat gcg gcc atg ctg cgc   576
Leu Leu Pro Leu Leu Ala Thr Cys Ala Cys Tyr Ala Ala Met Leu Arg
            180                 185                 190

cac ctg ggc cgg gtc gcc cgc gca ggc gcc gtg cgg gcc aag gtc tcg   624
His Leu Gly Arg Val Ala Arg Ala Gly Ala Val Arg Ala Lys Val Ser
        195                 200                 205

cgg ctg gtg gcg gcc gtg gtc ctg ctc ttc gcc gcc tgc tgg ggc ccc   672
Arg Leu Val Ala Ala Val Val Leu Leu Phe Ala Ala Cys Trp Gly Pro
    210                 215                 220

atc cag ctg ttc ctg gtg ctg cag gcg ctg ggc ccc gcg ggc tcc tgg   720
Ile Gln Leu Phe Leu Val Leu Gln Ala Leu Gly Pro Ala Gly Ser Trp
225                 230                 235                 240
```

```
cac cca cgc agc tac gcc gcc tac gcg ctt aag acc tgg gct cac tgc   768
His Pro Arg Ser Tyr Ala Ala Tyr Ala Leu Lys Thr Trp Ala His Cys
                245                 250                 255

atg tcc tac agc aac tcc gcg ctg aac ccg ctg ctc tac gcc ttc ctg   816
Met Ser Tyr Ser Asn Ser Ala Leu Asn Pro Leu Leu Tyr Ala Phe Leu
            260                 265                 270

ggc tcg cac ttc cga cag gcc ttc cgc cgc gtc tgc ccc tgc gcg ccg   864
Gly Ser His Phe Arg Gln Ala Phe Arg Arg Val Cys Pro Cys Ala Pro
        275                 280                 285

cgc cgc ccc cgc cgc ccc cgc cgg ccc gga ccc tcg gac ccc gca gcc   912
Arg Arg Pro Arg Arg Pro Arg Arg Pro Gly Pro Ser Asp Pro Ala Ala
    290                 295                 300

cca cac gcg gag ctg ctc cgc ctg ggg tcc cac ccg gcc ccc gcc agg   960
Pro His Ala Glu Leu Leu Arg Leu Gly Ser His Pro Ala Pro Ala Arg
305                 310                 315                 320

gcg cag aag                                                       969
Ala Gln Lys
```

<210> 10
<211> 323
<212> PRT
<213> Homo sapiens

<400> 10

```
Arg Ala Val Asp Ala Trp Leu Val Pro Leu Phe Phe Ala Ala Leu Met
 1               5                  10                  15
Leu Leu Gly Leu Val Gly Asn Ser Leu Val Ile Tyr Val Ile Cys Arg
            20                  25                  30
His Lys Pro Met Arg Thr Val Thr Asn Phe Tyr Ile Ala Asn Leu Ala
        35                  40                  45
Ala Thr Asp Val Thr Phe Leu Leu Cys Cys Val Pro Phe Thr Ala Leu
    50                  55                  60
Leu Tyr Pro Leu Pro Gly Trp Val Leu Gly Asp Phe Met Cys Lys Phe
65                  70                  75                  80
Val Asn Tyr Ile Gln Gln Val Ser Val Gln Ala Thr Cys Ala Thr Leu
                85                  90                  95
Thr Ala Met Ser Val Asp Arg Trp Tyr Val Thr Val Phe Pro Leu Arg
            100                 105                 110
Ala Leu His Arg Arg Thr Pro Arg Leu Ala Leu Ala Val Ser Leu Ser
        115                 120                 125
Ile Trp Val Gly Ser Ala Ala Val Ser Ala Pro Val Leu Ala Leu His
    130                 135                 140
Arg Leu Ser Pro Gly Pro Arg Ala Tyr Cys Ser Glu Ala Phe Pro Ser
145                 150                 155                 160
Arg Ala Leu Glu Arg Ala Phe Ala Leu Tyr Asn Leu Leu Ala Leu Tyr
                165                 170                 175

Leu Leu Pro Leu Leu Ala Thr Cys Ala Cys Tyr Ala Ala Met Leu Arg
            180                 185                 190
His Leu Gly Arg Val Ala Arg Ala Gly Ala Val Arg Ala Lys Val Ser
        195                 200                 205
Arg Leu Val Ala Ala Val Val Leu Leu Phe Ala Ala Cys Trp Gly Pro
    210                 215                 220
Ile Gln Leu Phe Leu Val Leu Gln Ala Leu Gly Pro Ala Gly Ser Trp
225                 230                 235                 240
His Pro Arg Ser Tyr Ala Ala Tyr Ala Leu Lys Thr Trp Ala His Cys
```

```
                245                 250                 255
Met Ser Tyr Ser Asn Ser Ala Leu Asn Pro Leu Leu Tyr Ala Phe Leu
            260                 265                 270
Gly Ser His Phe Arg Gln Ala Phe Arg Arg Val Cys Pro Cys Ala Pro
        275                 280                 285
Arg Arg Pro Arg Arg Pro Arg Arg Pro Gly Pro Ser Asp Pro Ala Ala
    290                 295                 300
Pro His Ala Glu Leu Leu Arg Leu Gly Ser His Pro Ala Pro Ala Arg
305                 310                 315                 320
Ala Gln Lys
```

<210> 11
<211> 1005
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1005)

<400> 11

```
gct gcc ctg gaa aag tac tac ctt tcc att ttt tat ggg att gag ttc   48
Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile Glu Phe
 1               5                  10                  15

gtt gtg gga gtc ctt gga aat acc att gtt gtt tac ggc tac atc ttc   96
Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr Ile Phe
            20                  25                  30

tct ctg aag aac tgg aac agc agt aat att tat ctc ttt aac ctc tct   144
Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn Leu Ser
        35                  40                  45

gtc tct gac tta gct ttt ctg tgc acc ctc ccc atg ctg ata agg agt   192
Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile Arg Ser
    50                  55                  60

tat gcc aat gga aac tgg ata tat gga gac gtg ctc tgc ata agc aac   240
Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn
65                  70                  75                  80

cga tat gtg ctt cat gcc aac ctc tat acc agc att ctc ttt ctc act   288
Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe Leu Thr
                85                  90                  95

ttt atc agc ata gat cga tac ttg ata att aag tat cct ttc cga gaa   336
Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe Arg Glu
            100                 105                 110



cac ctt ctg caa aag aaa gag ttt gct att tta atc tcc ttg gcc att   384
His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu Ala Ile
        115                 120                 125

tgg gtt tta gta acc tta gag tta cta ccc ata ctt ccc ctt ata aat   432
Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu Ile Asn
    130                 135                 140

cct gtt ata act gac aat ggc acc acc tgt aat gat ttt gca agt tct   480
Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala Ser Ser
```

```
145                 150                 155                 160

gga gac ccc aac tac aac ctc att tac agc atg tgt cta aca ctg ttg   528
Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr Leu Leu
                165                 170                 175

ggg ttc ctt att cct ctt ttt gtg atg tgt ttc ttt tat tac aag att   576
Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr Lys Ile
            180                 185                 190

gct ctc ttc cta aag cag agg aat agg cag gtt gct act gct ctg ccc   624
Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala Leu Pro
        195                 200                 205

ctt gaa aag cct ctc aac ttg gtc atc atg gca gtg gta atc ttc tct   672
Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile Phe Ser
    210                 215                 220

gtg ctt ttt aca ccc tat cac gtc atg cgg aat gtg agg atc gct tca   720
Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile Ala Ser
225                 230                 235                 240

cgc ctg ggg agt tgg aag cag tat cag tgc act cag gtc gtc atc aac   768
Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val Ile Asn
                245                 250                 255

tcc ttt tac att gtg aca cgg cct ttg gcc ttt ctg aac agt gtc atc   816
Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser Val Ile
            260                 265                 270

aac cct gtc ttc tat ttt ctt ttg gga gat cac ttc agg gac atg ctg   864
Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp Met Leu
        275                 280                 285

atg aat caa ctg aga cac aac ttc aaa tcc ctt aca tcc ttt agc aga   912
Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe Ser Arg
    290                 295                 300

tgg gct cat gaa ctc cta ctt tca ttc aga gaa aat gat tct cct tcc   960
Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Asn Asp Ser Pro Ser
305                 310                 315                 320

tca ccc tcc tca aat ggt gcg att aca gaa gtg agc cac cgc acg       1005
Ser Pro Ser Ser Asn Gly Ala Ile Thr Glu Val Ser His Arg Thr
                325                 330                 335
```

<210> 12
<211> 335
<212> PRT
<213> Homo sapiens

```
<400> 12
Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile Glu Phe
 1               5                  10                  15
Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr Ile Phe
            20                  25                  30
Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn Leu Ser
        35                  40                  45
Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile Arg Ser
    50                  55                  60
Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn
```

```
65                  70                  75                  80
Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe Leu Thr
                85                  90                  95
Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe Arg Glu
            100                 105                 110
His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu Ala Ile
        115                 120                 125
Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu Ile Asn
    130                 135                 140
Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala Ser Ser
145                 150                 155                 160
Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr Leu Leu
                165                 170                 175
Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr Lys Ile
            180                 185                 190
Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala Leu Pro
        195                 200                 205
Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile Phe Ser
    210                 215                 220
Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile Ala Ser
225                 230                 235                 240
Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val Ile Asn
                245                 250                 255
Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser Val Ile
            260                 265                 270
Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp Met Leu
        275                 280                 285
Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe Ser Arg
    290                 295                 300
Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Asn Asp Ser Pro Ser
305                 310                 315                 320
Ser Pro Ser Ser Asn Gly Ala Ile Thr Glu Val Ser His Arg Thr
                325                 330                 335
```

<210> 13
<211> 930
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(930)

<400> 13

```
aac ttg cct ctt cag atc acc ctt tct gct ata atg ata ttc att ctg   48
Asn Leu Pro Leu Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu
 1               5                  10                  15

ttt gtg tct ttt ctt ggg aac ttg gtt gtt tgc ctc atg gtt tac caa   96
Phe Val Ser Phe Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln
             20                  25                  30

aaa gct gcc atg agg tct gca att aac atc ctc ctt gcc agc cta gct   144
Lys Ala Ala Met Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala
         35                  40                  45

ttt gca gac atg ttg ctt gca gtg ctg aac atg ccc ttt gcc ctg gta   192
Phe Ala Asp Met Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val
     50                  55                  60

act att ctt act acc cga tgg att ttt ggg aaa ttc ttc tgt agg gta   240
Thr Ile Leu Thr Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val
```

```
 65                  70                  75                  80

tct gct atg ttt ttc tgg tta ttt gtg ata gaa gga gta gcc atc ctg   288
Ser Ala Met Phe Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu
                 85                  90                  95

ctc atc att agc ata gat agg ttc ctt att ata gtc cag agg cag gat   336
Leu Ile Ile Ser Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp
            100                 105                 110

aag cta aac cca tat aga gct aag gtt ctg att gca gtt tct tgg gca   384
Lys Leu Asn Pro Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala
        115                 120                 125

act tcc ttt tgt gta gct ttt cct tta gcc gta gga aac ccc gac ctg   432
Thr Ser Phe Cys Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu
    130                 135                 140

cag ata cct tcc cga gct ccc cag tgt gtg ttt ggg tac aca acc aat   480
Gln Ile Pro Ser Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn
145                 150                 155                 160

cca ggc tac cag gct tat gtg att ttg att tct ctc att tct ttc ttc   528
Pro Gly Tyr Gln Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe
                165                 170                 175

ata ccc ttc ctg gta ata cta cct ttc cag atg agc att gac atg ggc   576
Ile Pro Phe Leu Val Ile Leu Pro Phe Gln Met Ser Ile Asp Met Gly
            180                 185                 190

ttt aaa aca cgt gcc ttc acc act att ttg att ctc ttt gct gtc ttc   624
Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe Ala Val Phe
        195                 200                 205

att gtc tgc tgg gcc cca ttc acc act tac agc ctt gtg gca aca ttc   672
Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val Ala Thr Phe
    210                 215                 220

agt aag cac ttt tac tat cag cac aac ttt ttt gag att agc acc tgg   720
Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile Ser Thr Trp
225                 230                 235                 240

cta ctg tgg ctc tgc tac ctc aag tct gca ttg aat ccg ctg atc tac   768
Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro Leu Ile Tyr
                245                 250                 255

tac tgg agg att aag aaa ttc cat gat gct tgc ctg gac atg atg cct   816
Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp Met Met Pro
            260                 265                 270


aag tcc ttc aag ttt ttg ccg cag ctc cct ggt cac aca aag cga cgg   864
Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr Lys Arg Arg
        275                 280                 285

ata cat ttt aca cac aca cac aca cac aca cac aca cac aca cac acg   912
Ile His Phe Thr His Thr His Thr His Thr His Thr His Thr His Thr
    290                 295                 300

cac aca cag aaa cac atg                                          930
His Thr Gln Lys His Met
305                 310
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<210> 14
<211> 310
<212> PRT
<213> Homo sapiens

<400> 14
Asn Leu Pro Leu Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu
1 5 10 15
Phe Val Ser Phe Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln
20 25 30
Lys Ala Ala Met Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala
35 40 45
Phe Ala Asp Met Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val
50 55 60
Thr Ile Leu Thr Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val
65 70 75 80
Ser Ala Met Phe Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu
85 90 95
Leu Ile Ile Ser Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp
100 105 110
Lys Leu Asn Pro Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala
115 120 125
Thr Ser Phe Cys Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu
130 135 140
Gln Ile Pro Ser Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn
145 150 155 160
Pro Gly Tyr Gln Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe
165 170 175
Ile Pro Phe Leu Val Ile Leu Pro Phe Gln Met Ser Ile Asp Met Gly
180 185 190
Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe Ala Val Phe
195 200 205
Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val Ala Thr Phe
210 215 220
Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile Ser Thr Trp
225 230 235 240
Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro Leu Ile Tyr
245 250 255
Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp Met Met Pro
260 265 270
Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr Lys Arg Arg
275 280 285
Ile His Phe Thr His Thr His Thr His Thr His Thr His Thr His Thr
290 295 300
His Thr Gln Lys His Met
305 310

<210> 15
<211> 951
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(951)

<400> 15
agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg gtt atc ttc ctc 48
Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu Val Ile Phe Leu
1 5 10 15

gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta gtg ttg cag cgc 96

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Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu Val Leu Gln Arg
             20                  25                  30

aag ccg cag ctg ctg cag gtg acc aac cgt ttt atc ttt aac ctc ctc   144
Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile Phe Asn Leu Leu
         35                  40                  45

gtc acc gac ctg ctg cag att tcg ctc gtg gcc ccc tgg gtg gtg gcc   192
Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro Trp Val Val Ala
     50                  55                  60

acc tct gtg cct ctc ttc tgg ccc ctc aac agc cac ttc tgc acg gcc   240
Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His Phe Cys Thr Ala
 65                  70                  75                  80

ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc gtc aac acc att   288
Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser Val Asn Thr Ile
                 85                  90                  95

gtc gtg gtg tca gtg gat cgc tac ttg tcc atc atc cac cct ctc tcc   336
Val Val Val Ser Val Asp Arg Tyr Leu Ser Ile Ile His Pro Leu Ser
            100                 105                 110

tac ccg tcc aag atg acc cag cgc cgc ggt tac ctg ctc ctc tat ggc   384
Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly
        115                 120                 125

acc tgg att gtg gcc atc ctg cag agc act cct cca ctc tac ggc tgg   432
Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp
    130                 135                 140

ggc cag gct gcc ttt gat gag cgc aat gct ctc tgc tcc atg atc tgg   480
Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys Ser Met Ile Trp
145                 150                 155                 160

ggg gcc agc ccc agc tac act att ctc agc gtg gtg tcc ttc atc gtc   528
Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val Ser Phe Ile Val
                165                 170                 175

att cca ctg att gtc atg att gcc tgc tac tcc gtg gtg ttc tgt gca   576
Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val Val Phe Cys Ala
            180                 185                 190

gcc cgg agg cag cat gct ctg ctg tgc tac cag tgc aaa gct gct aaa   624
Ala Arg Arg Gln His Ala Leu Leu Cys Tyr Gln Cys Lys Ala Ala Lys
        195                 200                 205


gtg atc ttc atc atc att ttc tcc tat gtg cta tcc ctg ggg ccc tac   672
Val Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr
    210                 215                 220

tgc ttt tta gca gtc ctg gcc gtg tgg gtg gat gtc gaa acc cag gta   720
Cys Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val
225                 230                 235                 240

ccc cag tgg gtg atc acc ata atc atc tgg ctt ttc ttc ctg cag tgc   768
Pro Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys
                245                 250                 255

tgc atc cac ccc tat gtc tat ggc tac atg cac aag acc att aag aag   816
Cys Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys
            260                 265                 270
```

```
gaa atc cag gac atg ctg aag aaa caa cta aac cag cag tct tca tct   864
Glu Ile Gln Asp Met Leu Lys Lys Gln Leu Asn Gln Gln Ser Ser Ser
        275                 280                 285

gac tct ggc tcc tcc tcc tct tca gaa gat gaa cga ccc atg aga tcc   912
Asp Ser Gly Ser Ser Ser Ser Ser Glu Asp Glu Arg Pro Met Arg Ser
    290                 295                 300

cat gtg aag aat ggt gag gtt ggc agg cgg cgg aga cat               951
His Val Lys Asn Gly Glu Val Gly Arg Arg Arg Arg His
305                 310                 315
```

<210> 16
<211> 317
<212> PRT
<213> Homo sapiens

<400> 16

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Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu Val Ile Phe Leu
 1               5                  10                  15
Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu Val Leu Gln Arg
            20                  25                  30
Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile Phe Asn Leu Leu
        35                  40                  45
Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro Trp Val Val Ala
    50                  55                  60
Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His Phe Cys Thr Ala
65                  70                  75                  80
Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser Val Asn Thr Ile
                85                  90                  95
Val Val Val Ser Val Asp Arg Tyr Leu Ser Ile Ile His Pro Leu Ser
            100                 105                 110
Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly
        115                 120                 125
Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp
    130                 135                 140
Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys Ser Met Ile Trp
145                 150                 155                 160
Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val Ser Phe Ile Val
                165                 170                 175
Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val Val Phe Cys Ala
            180                 185                 190
Ala Arg Arg Gln His Ala Leu Leu Cys Tyr Gln Cys Lys Ala Ala Lys
        195                 200                 205

Val Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr
    210                 215                 220
Cys Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val
225                 230                 235                 240
Pro Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys
                245                 250                 255
Cys Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys
            260                 265                 270
Glu Ile Gln Asp Met Leu Lys Lys Gln Leu Asn Gln Gln Ser Ser Ser
        275                 280                 285
Asp Ser Gly Ser Ser Ser Ser Ser Glu Asp Glu Arg Pro Met Arg Ser
    290                 295                 300
His Val Lys Asn Gly Glu Val Gly Arg Arg Arg Arg His
305                 310                 315
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<210> 17
<211> 951
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(951)

<400> 17

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ccg gga cgc gcc aag atg gcc ctc gtg ctc acc ggc gtg ctc ata ttc   48
Pro Gly Arg Ala Lys Met Ala Leu Val Leu Thr Gly Val Leu Ile Phe
 1               5                  10                  15

gcc ctg gcg ctc ttt ggc aat gct ctg gtg ttt tac gtg gtg acc cgc   96
Ala Leu Ala Leu Phe Gly Asn Ala Leu Val Phe Tyr Val Val Thr Arg
            20                  25                  30

agc aag acc atg cgc acc gtc acc aac atc ttt ata tgc tcc ctg gcg   144
Ser Lys Thr Met Arg Thr Val Thr Asn Ile Phe Ile Cys Ser Leu Ala
        35                  40                  45

ctc agt gac atg ctc atc acc ctc ttt tgc att ccc gtc acc atg ctc   192
Leu Ser Asp Met Leu Ile Thr Leu Phe Cys Ile Pro Val Thr Met Leu
    50                  55                  60

cag aac att tcc gac aac tgg ctg ggg ggt gct ttc att tgc aag atg   240
Gln Asn Ile Ser Asp Asn Trp Leu Gly Gly Ala Phe Ile Cys Lys Met
65                  70                  75                  80

gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg   288
Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu Ile Leu Thr Met
                85                  90                  95

acc tgc att gct gtg gaa agg cac cag gga ctt gtg cat cct ttt aaa   336
Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val His Pro Phe Lys
            100                 105                 110

atg aag tgg caa tac acc aac cga agg gct ttc aca atg cta ggt gtg   384
Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr Met Leu Gly Val
        115                 120                 125

gtc tgg ctg gtg gca gtc atc gta gga tca ccc atg tgg cac atc aaa   432
Val Trp Leu Val Ala Val Ile Val Gly Ser Pro Met Trp His Ile Lys
    130                 135                 140

tat gac ttc cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg   480
Tyr Asp Phe Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp
145                 150                 155                 160

acc agc cct gtg cac cag aag atc tac acc acc ttc atc ctt gtc atc   528
Thr Ser Pro Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile
                165                 170                 175

ctc ttc ctc ctg cct ctt atg gtg atg ctt att ctg tac agt aaa att   576
Leu Phe Leu Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile
            180                 185                 190

ggt tat gaa ctt tgg ata aag aaa aga aag aaa cga gct gtc att atg   624
Gly Tyr Glu Leu Trp Ile Lys Lys Arg Lys Lys Arg Ala Val Ile Met
        195                 200                 205

atg gtg aca gtg gtg gct ctc ttt gct gtg tgc tgg gca cca ttc cat   672
```

```
Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro Phe His
    210                 215                 220

gtt gtc cat atg atg att gaa tac agt gaa ttc ctc tcc cat gtt act   720
Val Val His Met Met Ile Glu Tyr Ser Glu Phe Leu Ser His Val Thr
225                 230                 235                 240

cct tct atg att ttt gct atc gtg caa att att gga ttt tcc aac tcc   768
Pro Ser Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser
                245                 250                 255

atc tgt aat ccc att gtc tat gca ttt atg aat gaa aac ttc aaa aaa   816
Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys
            260                 265                 270

aat gtt ttg tct gca gtt tgt tat tgc ata gta aat aaa acc ttc tct   864
Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser
        275                 280                 285

cca gca caa agg cat gga aat tca gga att aca atg atg cgg aag aaa   912
Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys
    290                 295                 300

gca aag ttt tcc ctc aga gag aat cca gtg gag gaa acc               951
Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu Glu Thr
305                 310                 315


<210> 18
<211> 317
<212> PRT
<213> Homo sapiens

<400> 18
Pro Gly Arg Ala Lys Met Ala Leu Val Leu Thr Gly Val Leu Ile Phe
 1               5                  10                  15
Ala Leu Ala Leu Phe Gly Asn Ala Leu Val Phe Tyr Val Val Thr Arg
            20                  25                  30
Ser Lys Thr Met Arg Thr Val Thr Asn Ile Phe Ile Cys Ser Leu Ala
        35                  40                  45
Leu Ser Asp Met Leu Ile Thr Leu Phe Cys Ile Pro Val Thr Met Leu
    50                  55                  60
Gln Asn Ile Ser Asp Asn Trp Leu Gly Gly Ala Phe Ile Cys Lys Met
65                  70                  75                  80

Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu Ile Leu Thr Met
                85                  90                  95
Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val His Pro Phe Lys
            100                 105                 110
Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr Met Leu Gly Val
        115                 120                 125
Val Trp Leu Val Ala Val Ile Val Gly Ser Pro Met Trp His Ile Lys
    130                 135                 140
Tyr Asp Phe Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp
145                 150                 155                 160
Thr Ser Pro Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile
                165                 170                 175
Leu Phe Leu Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile
            180                 185                 190
Gly Tyr Glu Leu Trp Ile Lys Lys Arg Lys Lys Arg Ala Val Ile Met
        195                 200                 205
Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro Phe His
    210                 215                 220
```

```
Val Val His Met Met Ile Glu Tyr Ser Glu Phe Leu Ser His Val Thr
225                 230                 235                 240
Pro Ser Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser
                245                 250                 255
Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys
            260                 265                 270
Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser
        275                 280                 285
Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys
    290                 295                 300
Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu Glu Thr
305                 310                 315


<210> 19
<211> 999
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(999)

<400> 19
ttc ttc gca gcc aag atc gtc att ggc att gca ctg gca ggc atc atg   48
Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met
 1               5                  10                  15

ctg gtc tgc ggc atc ggt aac ttt gtc ttt atc gct gcc ctc acc cgc   96
Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg
            20                  25                  30

tat aag aag ttg cgc aac ctc acc aat ctg ctc att gcc aac ctg gcc   144
Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala
        35                  40                  45

atc tcc gac ttc ctg gtg gcc atc atc tgc tgc ccc ttc gag atg gac   192
Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp
    50                  55                  60

tac tac gtg gta cgg cag ctc tcc tgg gag cat ggc cac gtg ctc tgt   240
Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys
65                  70                  75                  80

gcc tcc gtc aac tac ctg cgc acc gtc tcc ctc tac gtc tcc acc aat   288
Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn
                85                  90                  95

gcc ttg ctg gcc att gcc att gac aga tat ctc gcc atc gtt cac ccc   336
Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro
            100                 105                 110

ttg aaa cca cgg atg aat tat caa acg gcc tcc ttc ctg atc gcc ttg   384
Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu
        115                 120                 125

gtc tgg atg gtg tcc att ctc att gcc atc cca tcg gct tac ttt gca   432
Val Trp Met Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala
    130                 135                 140

aca gaa acg gtc ctc ttt att gtc aag agc cag gag aag atc ttc tgt   480
Thr Glu Thr Val Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys
145                 150                 155                 160
```

```
ggc cag atc tgg cct gtg gat cag cag ctc tac tac aag tcc tac ttc   528
Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe
                165                 170                 175

ctc ttc atc ttt ggt gtc gag ttc gtg ggc cct gtg gtc acc atg acc   576
Leu Phe Ile Phe Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr
            180                 185                 190

ctg tgc tat gcc agg atc tcc cgg gag ctc tgg ttc aag gca att cgc   624
Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Ile Arg
        195                 200                 205

aag cgg ctg cgc tgc cgc agg aag acg gtc ctg gtg ctc atg tgc att   672
Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys Ile
    210                 215                 220

ctc acg gcc tat gtg ctg tgc tgg gca ccc ttc tac ggt ttc acc atc   720
Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr Ile
225                 230                 235                 240

gtt cgt gac ttc ttc ccc act gtg ttc gtg aag gaa aag cac tac ctc   768
Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr Leu
                245                 250                 255

act gcc ttc tac gtg gtc gag tgc atc gcc atg agc aac agc atg atc   816
Thr Ala Phe Tyr Val Val Glu Cys Ile Ala Met Ser Asn Ser Met Ile
            260                 265                 270

aac acc gtc cca ttt ttg tat ttt tgg ttg aga tgg ggc ttc act ata   864
Asn Thr Val Pro Phe Leu Tyr Phe Trp Leu Arg Trp Gly Phe Thr Ile
        275                 280                 285

ttt ctc agg ctg act ctg tct caa aaa aaa aaa aaa aga aga aga aga   912
Phe Leu Arg Leu Thr Leu Ser Gln Lys Lys Lys Lys Arg Arg Arg Arg
    290                 295                 300

aaa aga aaa aga act gaa agc aga gac tca aac aga tat ttg tac act   960
Lys Arg Lys Arg Thr Glu Ser Arg Asp Ser Asn Arg Tyr Leu Tyr Thr
305                 310                 315                 320


cat gtt cct agc agc att att cac agc act cca gcc tgg               999
His Val Pro Ser Ser Ile Ile His Ser Thr Pro Ala Trp
                325                 330
```

<210> 20
<211> 333
<212> PRT
<213> Homo sapiens

<400> 20

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Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met
 1               5                  10                  15
Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg
            20                  25                  30
Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala
        35                  40                  45
Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp
    50                  55                  60
Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys
```

```
65                  70                  75                  80
Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn
                85                  90                  95
Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro
            100                 105                 110
Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu
        115                 120                 125
Val Trp Met Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala
    130                 135                 140
Thr Glu Thr Val Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys
145                 150                 155                 160
Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe
                165                 170                 175
Leu Phe Ile Phe Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr
            180                 185                 190
Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Ile Arg
        195                 200                 205
Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys Ile
    210                 215                 220
Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr Ile
225                 230                 235                 240
Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr Leu
                245                 250                 255
Thr Ala Phe Tyr Val Val Glu Cys Ile Ala Met Ser Asn Ser Met Ile
            260                 265                 270
Asn Thr Val Pro Phe Leu Tyr Phe Trp Leu Arg Trp Gly Phe Thr Ile
        275                 280                 285
Phe Leu Arg Leu Thr Leu Ser Gln Lys Lys Lys Lys Arg Arg Arg Arg
    290                 295                 300
Lys Arg Lys Arg Thr Glu Ser Arg Asp Ser Asn Arg Tyr Leu Tyr Thr
305                 310                 315                 320
His Val Pro Ser Ser Ile Ile His Ser Thr Pro Ala Trp
                325                 330
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<210> 21
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(948)

<400> 21

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tcc tgg gaa cta cag atg ttt ttc ttt atg gtg ttt tca ttg ctt tat   48
Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser Leu Leu Tyr
 1               5                  10                  15

gtg gca aca atg gtg ggt aac agc ctc ata gtc atc aca gtt ata gtg   96
Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr Val Ile Val
             20                  25                  30

gac cct cac cta cac tct cct atg tat ttc ctg ctt acc aat ctt tca   144
Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr Asn Leu Ser
         35                  40                  45

atc att gat atg tct ctt gct tct ttc gcc acc cca aag atg att aca   192
Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys Met Ile Thr
     50                  55                  60

gat tac cta aca ggt cac aaa acc atc tct ttt gat ggc tgc ctt acc   240
Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly Cys Leu Thr
```

```
65                  70                  75                  80

cag ata ttc ttt ctc cac ctt ttc act gga act gag atc atc tta ctc   288
Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile Ile Leu Leu
                85                  90                  95

atg gcc atg tcc ttt gat agg tat att gca ata tgc aag ccc ctg cac   336
Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His
            100                 105                 110

tat gct tct gtc att agt ccc cag gtg tgt gtt gct ctc gtg gtg gct   384
Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu Val Val Ala
        115                 120                 125

tcc tgg att atg gga gtt atg cat tca atg aca cca ttt att gaa tat   432
Ser Trp Ile Met Gly Val Met His Ser Met Thr Pro Phe Ile Glu Tyr
    130                 135                 140

tta ttg att aga gtg tcc ttt ctc cat tgc ttg tct ttg ttg act tta   480
Leu Leu Ile Arg Val Ser Phe Leu His Cys Leu Ser Leu Leu Thr Leu
145                 150                 155                 160

cta aag aac agc tgg tta cag gta cgt ggc ttt gtt ttt ggg ttc tgt   528
Leu Lys Asn Ser Trp Leu Gln Val Arg Gly Phe Val Phe Gly Phe Cys
                165                 170                 175

att ctg ttc tat tgt cta tct ttc act ttc tct ctc ttg gtc agc tcc   576
Ile Leu Phe Tyr Cys Leu Ser Phe Thr Phe Ser Leu Leu Val Ser Ser
            180                 185                 190

tac atc att att ctt gtt aca gtt tgg ctc aag tct tca gct gca atg   624
Tyr Ile Ile Ile Leu Val Thr Val Trp Leu Lys Ser Ser Ala Ala Met
        195                 200                 205

gca aag gca ttt tct acg ctg gct tcc cat att gca gta gta ata tta   672
Ala Lys Ala Phe Ser Thr Leu Ala Ser His Ile Ala Val Val Ile Leu
    210                 215                 220

ttc ttt gga cct tgc atc ttc atc tat gtg tgg ccc ttt acc atc tct   720
Phe Phe Gly Pro Cys Ile Phe Ile Tyr Val Trp Pro Phe Thr Ile Ser
225                 230                 235                 240

cct ttg gat aaa ttt ctt gcc ata ttt tac act gtt ttc acc ccc gtc   768
Pro Leu Asp Lys Phe Leu Ala Ile Phe Tyr Thr Val Phe Thr Pro Val
                245                 250                 255

cta aac ccc att att tat aca cta agg aat agg gat atg aag gct gcc   816
Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Ala Ala
            260                 265                 270

gta agg aaa att agg act tca ata tct cac ttt cgg caa agg aca gat   864
Val Arg Lys Ile Arg Thr Ser Ile Ser His Phe Arg Gln Arg Thr Asp
        275                 280                 285

cat cta gac aaa aat tca gcc aaa aaa aca aca aat aca aag cgc act   912
His Leu Asp Lys Asn Ser Ala Lys Lys Thr Thr Asn Thr Lys Arg Thr
    290                 295                 300

cta gat cat gtg gac cta cca gat agt cac aga aca                   948
Leu Asp His Val Asp Leu Pro Asp Ser His Arg Thr
305                 310                 315
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<210> 22
<211> 316
<212> PRT
<213> Homo sapiens

<400> 22
Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser Leu Leu Tyr
1 5 10 15
Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr Val Ile Val
20 25 30
Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr Asn Leu Ser
35 40 45
Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys Met Ile Thr
50 55 60
Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly Cys Leu Thr
65 70 75 80
Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile Ile Leu Leu
85 90 95
Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His
100 105 110
Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu Val Val Ala
115 120 125
Ser Trp Ile Met Gly Val Met His Ser Met Thr Pro Phe Ile Glu Tyr
130 135 140
Leu Leu Ile Arg Val Ser Phe Leu His Cys Leu Ser Leu Leu Thr Leu
145 150 155 160
Leu Lys Asn Ser Trp Leu Gln Val Arg Gly Phe Val Phe Gly Phe Cys
165 170 175
Ile Leu Phe Tyr Cys Leu Ser Phe Thr Phe Ser Leu Leu Val Ser Ser
180 185 190
Tyr Ile Ile Ile Leu Val Thr Val Trp Leu Lys Ser Ser Ala Ala Met
195 200 205
Ala Lys Ala Phe Ser Thr Leu Ala Ser His Ile Ala Val Val Ile Leu
210 215 220
Phe Phe Gly Pro Cys Ile Phe Ile Tyr Val Trp Pro Phe Thr Ile Ser
225 230 235 240
Pro Leu Asp Lys Phe Leu Ala Ile Phe Tyr Thr Val Phe Thr Pro Val
245 250 255
Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Ala Ala
260 265 270
Val Arg Lys Ile Arg Thr Ser Ile Ser His Phe Arg Gln Arg Thr Asp
275 280 285
His Leu Asp Lys Asn Ser Ala Lys Lys Thr Thr Asn Thr Lys Arg Thr
290 295 300
Leu Asp His Val Asp Leu Pro Asp Ser His Arg Thr
305 310 315

<210> 23
<211> 954
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(954)

<400> 23
agt gtg gta gat aca gtc atc ctc cct tcc atg att ggg att atc tgt 48
Ser Val Val Asp Thr Val Ile Leu Pro Ser Met Ile Gly Ile Ile Cys
1 5 10 15

tca aca ggg ctg gtt ggc aac atc ctc att gta ttc act ata ata aga 96

```
Ser Thr Gly Leu Val Gly Asn Ile Leu Ile Val Phe Thr Ile Ile Arg
             20                  25                  30

tcc agg aaa aaa aca gtc cct gac atc tat atc tgc aac ctg gct gtg   144
Ser Arg Lys Lys Thr Val Pro Asp Ile Tyr Ile Cys Asn Leu Ala Val
         35                  40                  45

gct gat ttg gtc cac ata gtt gga atg cct ttt ctt att cac caa tgg   192
Ala Asp Leu Val His Ile Val Gly Met Pro Phe Leu Ile His Gln Trp
     50                  55                  60

gcc cga ggg gga gag tgg gtg ttt ggg ggg cct ctc tgc acc atc atc   240
Ala Arg Gly Gly Glu Trp Val Phe Gly Gly Pro Leu Cys Thr Ile Ile
 65                  70                  75                  80

aca tcc ctg gat act tgt aac caa ttt gcc tgt agt gcc atc atg act   288
Thr Ser Leu Asp Thr Cys Asn Gln Phe Ala Cys Ser Ala Ile Met Thr
                 85                  90                  95

gta atg agt gtg gac agg tac ttt gcc ctc gtc caa cca ttt cga ctg   336
Val Met Ser Val Asp Arg Tyr Phe Ala Leu Val Gln Pro Phe Arg Leu
            100                 105                 110

aca cgt tgg aga aca agg tac aag acc atc cgg atc aat ttg ggc ctt   384
Thr Arg Trp Arg Thr Arg Tyr Lys Thr Ile Arg Ile Asn Leu Gly Leu
        115                 120                 125

tgg gca gct tcc ttt atc ctg gca ttg cct gtc tgg gtc tac tcg aag   432
Trp Ala Ala Ser Phe Ile Leu Ala Leu Pro Val Trp Val Tyr Ser Lys
    130                 135                 140

gtc atc aaa ttt aaa gac ggt gtt gag agt tgt ttg tca aat ttg ctt   480
Val Ile Lys Phe Lys Asp Gly Val Glu Ser Cys Leu Ser Asn Leu Leu
145                 150                 155                 160

atc ttt tca aag aaa tat ttt att tct ttg atc ttt tgt att att ttc   528
Ile Phe Ser Lys Lys Tyr Phe Ile Ser Leu Ile Phe Cys Ile Ile Phe
                165                 170                 175

ttt att tca att tca ttt att tct gct ctg atc ttt att aca ttt ctt   576
Phe Ile Ser Ile Ser Phe Ile Ser Ala Leu Ile Phe Ile Thr Phe Leu
            180                 185                 190

cta cta ttc tta gaa aaa caa caa caa caa aaa aaa aaa cac acg tca   624
Leu Leu Phe Leu Glu Lys Gln Gln Gln Gln Lys Lys Lys His Thr Ser
        195                 200                 205

cag gtc atg cat ctc cta ctc ttg tct tcc aca ttc ctt gta agt tgg   672
Gln Val Met His Leu Leu Leu Leu Ser Ser Thr Phe Leu Val Ser Trp
    210                 215                 220

att cct agg tat ttt att ctc ttt gaa gca att gtg aat ggg agt tca   720
Ile Pro Arg Tyr Phe Ile Leu Phe Glu Ala Ile Val Asn Gly Ser Ser
225                 230                 235                 240

ctc atg att tgg ctc tct gtt tgt ctg tta ttg gtg tat aag aat gct   768
Leu Met Ile Trp Leu Ser Val Cys Leu Leu Leu Val Tyr Lys Asn Ala
                245                 250                 255

tgt gat ttt tgc acc att cat tat ttt gat gtt aaa tgt gtc ttt agg   816
Cys Asp Phe Cys Thr Ile His Tyr Phe Asp Val Lys Cys Val Phe Arg
            260                 265                 270
```

```
aga aat tac aga caa ttg tca aag aaa aaa agc cat gga agc ttt gtg   864
Arg Asn Tyr Arg Gln Leu Ser Lys Lys Lys Ser His Gly Ser Phe Val
        275                 280                 285

ccc aca acc caa aca gaa agt tta tcc tcc acc cca acc caa cac agg   912
Pro Thr Thr Gln Thr Glu Ser Leu Ser Ser Thr Pro Thr Gln His Arg
    290                 295                 300

aaa gtg gtt gtt ttt ggt ttg gcc aga cca cta tgg gct act           954
Lys Val Val Val Phe Gly Leu Ala Arg Pro Leu Trp Ala Thr
305                 310                 315
```

<210> 24
<211> 318
<212> PRT
<213> Homo sapiens

<400> 24

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Ser Val Val Asp Thr Val Ile Leu Pro Ser Met Ile Gly Ile Ile Cys
 1               5                  10                  15
Ser Thr Gly Leu Val Gly Asn Ile Leu Ile Val Phe Thr Ile Ile Arg
            20                  25                  30
Ser Arg Lys Lys Thr Val Pro Asp Ile Tyr Ile Cys Asn Leu Ala Val
        35                  40                  45
Ala Asp Leu Val His Ile Val Gly Met Pro Phe Leu Ile His Gln Trp
    50                  55                  60
Ala Arg Gly Gly Glu Trp Val Phe Gly Gly Pro Leu Cys Thr Ile Ile
65                  70                  75                  80
Thr Ser Leu Asp Thr Cys Asn Gln Phe Ala Cys Ser Ala Ile Met Thr
                85                  90                  95
Val Met Ser Val Asp Arg Tyr Phe Ala Leu Val Gln Pro Phe Arg Leu
            100                 105                 110
Thr Arg Trp Arg Thr Arg Tyr Lys Thr Ile Arg Ile Asn Leu Gly Leu
        115                 120                 125
Trp Ala Ala Ser Phe Ile Leu Ala Leu Pro Val Trp Val Tyr Ser Lys
    130                 135                 140
Val Ile Lys Phe Lys Asp Gly Val Glu Ser Cys Leu Ser Asn Leu Leu
145                 150                 155                 160
Ile Phe Ser Lys Lys Tyr Phe Ile Ser Leu Ile Phe Cys Ile Ile Phe
                165                 170                 175
Phe Ile Ser Ile Ser Phe Ile Ser Ala Leu Ile Phe Ile Thr Phe Leu
            180                 185                 190
Leu Leu Phe Leu Glu Lys Gln Gln Gln Gln Lys Lys Lys His Thr Ser
        195                 200                 205
Gln Val Met His Leu Leu Leu Leu Ser Ser Thr Phe Leu Val Ser Trp
    210                 215                 220
Ile Pro Arg Tyr Phe Ile Leu Phe Glu Ala Ile Val Asn Gly Ser Ser
225                 230                 235                 240
Leu Met Ile Trp Leu Ser Val Cys Leu Leu Leu Val Tyr Lys Asn Ala
                245                 250                 255
Cys Asp Phe Cys Thr Ile His Tyr Phe Asp Val Lys Cys Val Phe Arg
            260                 265                 270
Arg Asn Tyr Arg Gln Leu Ser Lys Lys Lys Ser His Gly Ser Phe Val
        275                 280                 285
Pro Thr Thr Gln Thr Glu Ser Leu Ser Ser Thr Pro Thr Gln His Arg
    290                 295                 300
Lys Val Val Val Phe Gly Leu Ala Arg Pro Leu Trp Ala Thr
305                 310                 315
```

<210> 25

<211> 957
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(957)

<400> 25

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tgg cct cat ctg gaa gta gtt ctc ttt gtg gtt atc ttg atc ttc tac   48
Trp Pro His Leu Glu Val Val Leu Phe Val Val Ile Leu Ile Phe Tyr
 1               5                  10                  15

ttg ata aca ctg ata gga aac ctg ttc atc atc atc ctg tca tac ctg   96
Leu Ile Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Ser Tyr Leu
            20                  25                  30

gac tcc cat ctc cac act ccc atg tac ttc ttc ctt tca aat ctc tca   144
Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser
        35                  40                  45

ttt ctg gat ctc tgc tac acc acc agc tct atc cct cag ttg ctg gtg   192
Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu Leu Val
    50                  55                  60

aat ctc tgg ggc ccg gaa aag acc atc tct tat gct ggt tgt aca gtt   240
Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ala Gly Cys Thr Val
65                  70                  75                  80

caa ctt tac ttt gtt ctc gca ctg gga acc gca gag tgt gtc cta ctg   288
Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr Ala Glu Cys Val Leu Leu
                85                  90                  95

gtg gtg atg tcc tat gat cgt tat gca gct gtg tgt aga cct ttg cat   336
Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro Leu His
            100                 105                 110

tac act gtc ctc atg cac cct cgt ttc tgc cgc ttg ttg gct gcg gct   384
Tyr Thr Val Leu Met His Pro Arg Phe Cys Arg Leu Leu Ala Ala Ala
        115                 120                 125

tct tgg gta aca ctt cat tcc tcc ttt act ttc tgg gta ccc ctt tgt   432
Ser Trp Val Thr Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys
    130                 135                 140

gga cat cgc cta gtg gat cac ttc ttc tgt gaa gtt cca gca ctt ctg   480
Gly His Arg Leu Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu
145                 150                 155                 160

cgt tta tca tgt gtt gac acc cat gca aat gag ctg acc ctc atg gtc   528
Arg Leu Ser Cys Val Asp Thr His Ala Asn Glu Leu Thr Leu Met Val
                165                 170                 175

atg agc tcc att ttt gtt ctc ata cct ctc att ctg att ctc act gcc   576
Met Ser Ser Ile Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ala
            180                 185                 190

tat ggt gcc att gcc cgg gct gta ctg agc atg caa tca acc act ggg   624
Tyr Gly Ala Ile Ala Arg Ala Val Leu Ser Met Gln Ser Thr Thr Gly
        195                 200                 205

ctt cag aaa gtg ttt agg aca tgt gga gcc cat ctt atg gtt gta tct   672
Leu Gln Lys Val Phe Arg Thr Cys Gly Ala His Leu Met Val Val Ser
```

```
    210                 215                 220

ctc ttt ttc att cca gtc atg tgc atg tat ctc cag cca cca tca gaa   720
Leu Phe Phe Ile Pro Val Met Cys Met Tyr Leu Gln Pro Pro Ser Glu
225                 230                 235                 240

aat tct cct gat cag ggc aag ttc att gcc ctc ttt tat act gtt gtc   768
Asn Ser Pro Asp Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val
                245                 250                 255

aca ccg agt ctt aat cct cta atc tac act ctc aga aac aag cat gta   816
Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys His Val
            260                 265                 270

aaa ggg gca gcg aag aga cta ttg ggt gcc tgc cgc ccc atg cag agc   864
Lys Gly Ala Ala Lys Arg Leu Leu Gly Ala Cys Arg Pro Met Gln Ser
        275                 280                 285

cag ccc aga act gtg agg tca agt ttc ttt gat aga aag gca aca ggt   912
Gln Pro Arg Thr Val Arg Ser Ser Phe Phe Asp Arg Lys Ala Thr Gly
    290                 295                 300

tgt gag cct ggc tcc tgt gtg agg act ccg gca gca cag act tgt       957
Cys Glu Pro Gly Ser Cys Val Arg Thr Pro Ala Ala Gln Thr Cys
305                 310                 315
```

<210> 26
<211> 319
<212> PRT
<213> Homo sapiens

<400> 26

```
Trp Pro His Leu Glu Val Val Leu Phe Val Val Ile Leu Ile Phe Tyr
 1               5                  10                  15
Leu Ile Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Ser Tyr Leu
            20                  25                  30
Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser
        35                  40                  45
Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu Leu Val
    50                  55                  60
Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ala Gly Cys Thr Val
65                  70                  75                  80
Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr Ala Glu Cys Val Leu Leu
                85                  90                  95
Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro Leu His
            100                 105                 110
Tyr Thr Val Leu Met His Pro Arg Phe Cys Arg Leu Leu Ala Ala Ala
        115                 120                 125
Ser Trp Val Thr Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys
    130                 135                 140
Gly His Arg Leu Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu
145                 150                 155                 160
Arg Leu Ser Cys Val Asp Thr His Ala Asn Glu Leu Thr Leu Met Val
                165                 170                 175
Met Ser Ser Ile Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ala
            180                 185                 190
Tyr Gly Ala Ile Ala Arg Ala Val Leu Ser Met Gln Ser Thr Thr Gly
        195                 200                 205
Leu Gln Lys Val Phe Arg Thr Cys Gly Ala His Leu Met Val Val Ser
    210                 215                 220
Leu Phe Phe Ile Pro Val Met Cys Met Tyr Leu Gln Pro Pro Ser Glu
```

```
225                 230                 235                 240
Asn Ser Pro Asp Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val
                245                 250                 255
Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys His Val
            260                 265                 270
Lys Gly Ala Ala Lys Arg Leu Leu Gly Ala Cys Arg Pro Met Gln Ser
        275                 280                 285
Gln Pro Arg Thr Val Arg Ser Ser Phe Phe Asp Arg Lys Ala Thr Gly
    290                 295                 300
Cys Glu Pro Gly Ser Cys Val Arg Thr Pro Ala Ala Gln Thr Cys
305                 310                 315
```

<210> 27
<211> 963
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(963)

<400> 27

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gtt cgt gtc gtg ccc cgc acc gtg ttt ttt ttg ttt ttt ttt ttg ttt   48
Val Arg Val Val Pro Arg Thr Val Phe Phe Leu Phe Phe Phe Leu Phe
 1               5                  10                  15

att ttg gtt ctt gtt tca aat atc ttg aca gtg atc atc ctc tcc cag   96
Ile Leu Val Leu Val Ser Asn Ile Leu Thr Val Ile Ile Leu Ser Gln
            20                  25                  30

ctg gtg gca aga aga cag aag tcc tcc tac aac tat ctc ttg gca ctc   144
Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn Tyr Leu Leu Ala Leu
        35                  40                  45

gct gct gcc gac atc ttg gtc ctc ttt ttc ata gtg ttt gtg gac ttc   192
Ala Ala Ala Asp Ile Leu Val Leu Phe Phe Ile Val Phe Val Asp Phe
    50                  55                  60

ctg ttg gaa gat ttc atc ttg aac atg cag atg cct cag gtc ccc gac   240
Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met Pro Gln Val Pro Asp
65                  70                  75                  80

aag atc ata gaa gtg ctg gaa ttc tca tcc atc cac acc tcc ata tgg   288
Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile His Thr Ser Ile Trp
                85                  90                  95

att act gta ccg tta acc att gac agg tat atc gct gtc tgc cac ccg   336
Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile Ala Val Cys His Pro
            100                 105                 110

ctc aag tac cac acg gtc tca tac cca gcc cgc acc cgg aaa gtc att   384
Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg Thr Arg Lys Val Ile
        115                 120                 125

gta agt gtt tac atc acc tgc ttc ctg acc agc atc ccc tat tac tgg   432
Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser Ile Pro Tyr Tyr Trp
    130                 135                 140

tgg ccc aac atc tgg act gaa gac tac atc agc acc tct gtg cat cac   480
Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser Thr Ser Val His His
145                 150                 155                 160
```

```
gtc ctc atc tgg atc cac tgc ttc acc gtc tac ctg gtg ccc tgc tcc   528
Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr Leu Val Pro Cys Ser
                165                 170                 175

atc ttc ttc atc ttg aac tca atc att gtg tac aag ctc agg agg aag   576
Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr Lys Leu Arg Arg Lys
            180                 185                 190

agc aat ttt cgt ctc cgt ggc tac tcc acg ggg aag acc acc gcc atc   624
Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly Lys Thr Thr Ala Ile
        195                 200                 205

ttg ttc acc att acc tcc atc ttt gcc aca ctt tgg gcc ccc cgc atc   672
Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu Trp Ala Pro Arg Ile
    210                 215                 220

atc atg att ctt tac cac ctc tat ggg gcg ccc atc cag aac cgc tgg   720
Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro Ile Gln Asn Arg Trp
225                 230                 235                 240

ctg gta cac atc atg tcc gac att gcc aac atg cta gcc ctt ctg aac   768
Leu Val His Ile Met Ser Asp Ile Ala Asn Met Leu Ala Leu Leu Asn
                245                 250                 255

aca gcc atc aac ttc ttc ctc tac tgc ttc atc agc aag cgg ttc cgc   816
Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile Ser Lys Arg Phe Arg
            260                 265                 270

acc atg gca gcc gcc acg ctc aag gct ttc ttc aag tgc cag aag caa   864
Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe Lys Cys Gln Lys Gln
        275                 280                 285


cct gta caa att caa cct ttc aag cag ata tct tta agt cca aca cac   912
Pro Val Gln Ile Gln Pro Phe Lys Gln Ile Ser Leu Ser Pro Thr His
    290                 295                 300

aca cac aca cac aca cac aca cac aca cac aca cac act tct aaa gac   960
Thr His Thr His Thr His Thr His Thr His Thr His Thr Ser Lys Asp
305                 310                 315                 320

act                                                               963
Thr
```

<210> 28
<211> 321
<212> PRT
<213> Homo sapiens

```
<400> 28
Val Arg Val Val Pro Arg Thr Val Phe Phe Leu Phe Phe Phe Leu Phe
 1               5                  10                  15
Ile Leu Val Leu Val Ser Asn Ile Leu Thr Val Ile Ile Leu Ser Gln
            20                  25                  30
Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn Tyr Leu Leu Ala Leu
        35                  40                  45
Ala Ala Ala Asp Ile Leu Val Leu Phe Phe Ile Val Phe Val Asp Phe
    50                  55                  60
Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met Pro Gln Val Pro Asp
65                  70                  75                  80
```

```
Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile His Thr Ser Ile Trp
                85                  90                  95
Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile Ala Val Cys His Pro
            100                 105                 110
Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg Thr Arg Lys Val Ile
        115                 120                 125
Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser Ile Pro Tyr Tyr Trp
    130                 135                 140
Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser Thr Ser Val His His
145                 150                 155                 160
Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr Leu Val Pro Cys Ser
                165                 170                 175
Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr Lys Leu Arg Arg Lys
            180                 185                 190
Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly Lys Thr Thr Ala Ile
        195                 200                 205
Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu Trp Ala Pro Arg Ile
    210                 215                 220
Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro Ile Gln Asn Arg Trp
225                 230                 235                 240
Leu Val His Ile Met Ser Asp Ile Ala Asn Met Leu Ala Leu Leu Asn
                245                 250                 255
Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile Ser Lys Arg Phe Arg
            260                 265                 270
Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe Lys Cys Gln Lys Gln
        275                 280                 285
Pro Val Gln Ile Gln Pro Phe Lys Gln Ile Ser Leu Ser Pro Thr His
    290                 295                 300
Thr His Thr His Thr His Thr His Thr His Thr His Thr Ser Lys Asp
305                 310                 315                 320
Thr
```

<210> 29
<211> 969
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(969)

<400> 29

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atg ggc ccc ggc gag gcg ctg ctg gcg ggt ctc ctg gtg atg gta ctg   48
Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met Val Leu
 1               5                  10                  15

gcc gtg gcg ctg cta tcc aac gca ctg gtg ctg ctt tgt tgc gcc tac   96
Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys Ala Tyr
             20                  25                  30

agc gct gag ctc cgc act cga gcc tca ggc gtc ctc ctg gtg aat ctg   144
Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
         35                  40                  45

tct ctg ggc cac ctg ctg ctg gcg gcg ctg gac atg ccc ttc acg ctg   192
Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
     50                  55                  60

ctc ggt gtg atg cgc ggg cgg aca ccg tcg gcg ccc ggc gca tgc caa   240
Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
 65                  70                  75                  80
```

```
gtc att ggc ttc ctg gac acc ttc ctg gcg tcc aac gcg gcg ctg agc   288
Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
                 85                  90                  95

gtg gcg gcg ctg agc gca gac cag tgg ctg gca gtg ggc ttc cca ctg   336
Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
            100                 105                 110

cgc tac gcc gga cgc ctg cga ccg cgc tat gcc ggc ctg ctg ctg ggc   384
Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
        115                 120                 125

tgt gcc tgg gga cag tcg ctg gcc ttc tca ggc gct gca ctt ggc tgc   432
Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
    130                 135                 140

tcg tgg ctt ggc tac agc agc gcc ttc gcg tcc tgt tcg ctg cgc ctg   480
Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
145                 150                 155                 160

ccg ccc gag cct gag cgt ccg cgc ttc gca gcc ttc acc gcc acg ctc   528
Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
                165                 170                 175

cat gcc gtg ggc ttc gtg ctg ccg ctg gcg gtg ctc tgc ctc acc tcg   576
His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
            180                 185                 190

ctc cag gtg cac cgg gtg gca cgc aga cac tgc cag cgc atg gac acc   624
Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr
        195                 200                 205

cgg cgc cgc cac cgc gcc acc agg aag att ggc att gct att gcg acc   672
Arg Arg Arg His Arg Ala Thr Arg Lys Ile Gly Ile Ala Ile Ala Thr
    210                 215                 220

ttc ctc atc tgc ttt gcc ccg tat gtc atg acc agg ctg gcg gag ctc   720
Phe Leu Ile Cys Phe Ala Pro Tyr Val Met Thr Arg Leu Ala Glu Leu
225                 230                 235                 240

gtg ccc ttc gtc acc gtg aac gcc cag tgg ggc atc ctc agc aag tgc   768
Val Pro Phe Val Thr Val Asn Ala Gln Trp Gly Ile Leu Ser Lys Cys
                245                 250                 255

ctg acc tac agc aag gcg gtg gcc gac ccg ttc acg tac tct ctg ctc   816
Leu Thr Tyr Ser Lys Ala Val Ala Asp Pro Phe Thr Tyr Ser Leu Leu
            260                 265                 270

cgc cgg ccg ttc cgc caa gtc ctg gcc ggc atg gtg cac cgg ctg ctg   864
Arg Arg Pro Phe Arg Gln Val Leu Ala Gly Met Val His Arg Leu Leu
        275                 280                 285

aag aga acc ccg cgc cca gca tcc acc cat gac agc tct ctg gat gtg   912
Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asp Ser Ser Leu Asp Val
    290                 295                 300

gcc ggc atg gtg cac cag ctg ctg aag aga acc ccg cgc cca gcg tcc   960
Ala Gly Met Val His Gln Leu Leu Lys Arg Thr Pro Arg Pro Ala Ser
305                 310                 315                 320

acc cac aac                                                      969
Thr His Asn
```

<210> 30
<211> 323
<212> PRT
<213> Homo sapiens

<400> 30
Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met Val Leu
1 5 10 15
Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys Ala Tyr
20 25 30
Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
35 40 45
Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
50 55 60
Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
65 70 75 80
Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
85 90 95
Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
100 105 110
Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
115 120 125
Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
130 135 140
Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
145 150 155 160
Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
165 170 175

His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
180 185 190
Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr
195 200 205
Arg Arg Arg His Arg Ala Thr Arg Lys Ile Gly Ile Ala Ile Ala Thr
210 215 220
Phe Leu Ile Cys Phe Ala Pro Tyr Val Met Thr Arg Leu Ala Glu Leu
225 230 235 240
Val Pro Phe Val Thr Val Asn Ala Gln Trp Gly Ile Leu Ser Lys Cys
245 250 255
Leu Thr Tyr Ser Lys Ala Val Ala Asp Pro Phe Thr Tyr Ser Leu Leu
260 265 270
Arg Arg Pro Phe Arg Gln Val Leu Ala Gly Met Val His Arg Leu Leu
275 280 285
Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asp Ser Ser Leu Asp Val
290 295 300
Ala Gly Met Val His Gln Leu Leu Lys Arg Thr Pro Arg Pro Ala Ser
305 310 315 320
Thr His Asn

<210> 31
<211> 981
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(981)

<400> 31

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ttg gaa ggc atc aaa cac tgg att ttc atc ccc ttt ttc ttt atg tac   48
Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe Phe Phe Met Tyr
 1               5                  10                  15

atg gtt gcc atc tca ggc aat tgt ttc att ctg atc att att aag acc   96
Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile Ile Ile Lys Thr
            20                  25                  30

aac cct cgt ctg cac aca ccc atg tac tat cta cta tcc ttg ctg gcc   144
Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu Ser Leu Leu Ala
        35                  40                  45

ctc act gac ctg ggg ctg tgt gtg tcc acg ttg ccc acc act atg ggg   192
Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro Thr Thr Met Gly
    50                  55                  60

atc ttc tgg ttt aac tcc cag agt atc tac ttt gga gcg tgt caa atc   240
Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly Ala Cys Gln Ile
65                  70                  75                  80

cag atg ttc tgc atc cac tct ttt tcc ttc atg gag tcc tca gtg ctc   288
Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu Ser Ser Val Leu
                85                  90                  95

ctc atg atg tcc ttt gac cgc ttt gtg gcc atc tgc cac cct ctg agg   336
Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
            100                 105                 110


tat tcg gtc att atc act ggc cag caa gtg gtc aga gca ggc cta att   384
Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg Ala Gly Leu Ile
        115                 120                 125

gtc atc ttc cgg gga cct gtg gcc act atc cct att gtc ctc ctc ctg   432
Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile Val Leu Leu Leu
    130                 135                 140

aag gct ttt ccc tac tgt gga tct gtg gtc ctc tcc cac tca ttt tgc   480
Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser His Ser Phe Cys
145                 150                 155                 160

ctg cac cag gaa gtg ata cag ctg gcc tgc aca gat acc acc ttc aat   528
Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp Thr Thr Phe Asn
                165                 170                 175

aat ctg tat gga ctg atg gtg gta gtt ttc act gtg atg ctg gac ctg   576
Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val Met Leu Asp Leu
            180                 185                 190

gtg ctc atc gca ctg tcc tat gga ctc atc ctg cac aca gta gca ggc   624
Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His Thr Val Ala Gly
        195                 200                 205

ctg gcc tcc caa gag gag cag cgc cgt gcc ttt cag aca tgc acc gct   672
Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln Thr Cys Thr Ala
    210                 215                 220

cat ctc tgt gct gtg cta gta ttc ttt gtg ccc atg atg ggg ctg tcc   720
His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met Met Gly Leu Ser
225                 230                 235                 240

ctg gtg cac cgt ttt ggg aag cat gcc cca cct gct att cat ctt ctt   768
```

```
Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala Ile His Leu Leu
                245                 250                 255

atg gcc aat gtc tac ctt ttt gtg cct ccc atg ctt aac cca atc ata   816
Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu Asn Pro Ile Ile
            260                 265                 270

tac agc att aag acc aag gag atc cac cgt gcc att atc aaa ctc cta   864
Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile Ile Lys Leu Leu
        275                 280                 285

gaa tgc aga agt ctc agg agc caa tgc aat caa ctg gaa gaa agg gta   912
Glu Cys Arg Ser Leu Arg Ser Gln Cys Asn Gln Leu Glu Glu Arg Val
    290                 295                 300

tca gtg atg gaa gat gaa atg aat gaa atg aag caa gaa gag aag ttt   960
Ser Val Met Glu Asp Glu Met Asn Glu Met Lys Gln Glu Glu Lys Phe
305                 310                 315                 320

aga gaa aaa aga ata aaa aga                                      981
Arg Glu Lys Arg Ile Lys Arg
                325
```

<210> 32
<211> 327
<212> PRT
<213> Homo sapiens

<400> 32

```
Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe Phe Phe Met Tyr
 1               5                  10                  15
Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile Ile Ile Lys Thr
            20                  25                  30
Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu Ser Leu Leu Ala
        35                  40                  45
Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro Thr Thr Met Gly
    50                  55                  60
Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly Ala Cys Gln Ile
65                  70                  75                  80
Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu Ser Ser Val Leu
                85                  90                  95
Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
            100                 105                 110
Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg Ala Gly Leu Ile
        115                 120                 125
Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile Val Leu Leu Leu
    130                 135                 140
Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser His Ser Phe Cys
145                 150                 155                 160
Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp Thr Thr Phe Asn
                165                 170                 175
Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val Met Leu Asp Leu
            180                 185                 190
Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His Thr Val Ala Gly
        195                 200                 205
Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln Thr Cys Thr Ala
    210                 215                 220
His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met Met Gly Leu Ser
225                 230                 235                 240
Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala Ile His Leu Leu
                245                 250                 255
Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu Asn Pro Ile Ile
```

```
            260                 265                 270
Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile Ile Lys Leu Leu
        275                 280                 285
Glu Cys Arg Ser Leu Arg Ser Gln Cys Asn Gln Leu Glu Glu Arg Val
    290                 295                 300
Ser Val Met Glu Asp Glu Met Asn Glu Met Lys Gln Glu Glu Lys Phe
305                 310                 315                 320
Arg Glu Lys Arg Ile Lys Arg
                325
```

<210> 33
<211> 972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(972)

<400> 33

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cac agt act gct gac ctt gtc ctc ttc tcc gtg gtt atg gcg gtc ttc   48
His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val Met Ala Val Phe
 1               5                  10                  15

aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc ctc atc tac atg   96
Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe Leu Ile Tyr Met
            20                  25                  30

gac cct cac ctt cac acc ccc atg tac ttc ttc ctc agc cag ctc tcc   144
Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser
        35                  40                  45

ctc atg gac ctc atg ttg gtc tgt acc aat gtg cca aag atg gca gcc   192
Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro Lys Met Ala Ala
    50                  55                  60

aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg ggc tgt ggc ata   240
Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val Gly Cys Gly Ile
65                  70                  75                  80

caa att ggc ctc ttt gtc tgt ctt gtg gga tct gag ggg ctc ttg ctg   288
Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu Gly Leu Leu Leu
                85                  90                  95

gga ctc atg gct tat gac cgc tat gtg gcc att agc cac cca ctt cac   336
Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser His Pro Leu His
            100                 105                 110

tat ccc atc ctc atg aat cag agg gtc tgt ctc cag att act ggg agc   384
Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln Ile Thr Gly Ser
        115                 120                 125

tcc tgg gcc ttt ggg ata atc gat ggc ttg atc cag atg gtg gta gta   432
Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln Met Val Val Val
    130                 135                 140

atg aat ttc ccc tac tgt ggc ttg agg aag gtg aac cat ttc ttc tgt   480
Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn His Phe Phe Cys
145                 150                 155                 160

gag atg cta tcc ttg ttg aag ctg gcc tgt gtg ata ttt gct tgc tgt   528
Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Ile Phe Ala Cys Cys
```

```
                165                 170                 175

gtc ttc atg ctt ctc ttc cca ttc tcc atc atc gtg gcc tcc tat gct   576
Val Phe Met Leu Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala
            180                 185                 190

cac att cta ggg act gtg ctg caa atg cac tct gct cag gcc tgg aaa   624
His Ile Leu Gly Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys
        195                 200                 205

aag gcc ctg gcc acc tgc tcc tcc cac ctg aca gct ttt ttt ttt tgc   672
Lys Ala Leu Ala Thr Cys Ser Ser His Leu Thr Ala Phe Phe Phe Cys
    210                 215                 220

caa cta cct tac caa atc ctt tcc cat caa gtt gtc tgt tca ttt tat   720
Gln Leu Pro Tyr Gln Ile Leu Ser His Gln Val Val Cys Ser Phe Tyr
225                 230                 235                 240

tgg gtg att ttg ggg cat aga tgt gac aaa tct tca ttg caa tca agt   768
Trp Val Ile Leu Gly His Arg Cys Asp Lys Ser Ser Leu Gln Ser Ser
                245                 250                 255

aca gtg tca ctt tca ttt gcg gtt ctt aat cca att cta tat ggc agc   816
Thr Val Ser Leu Ser Phe Ala Val Leu Asn Pro Ile Leu Tyr Gly Ser
            260                 265                 270


gtc gcc cgc tcc ttt cgg cgc agg gcg gga gcc ctt ctt gtg tgc aga   864
Val Ala Arg Ser Phe Arg Arg Arg Ala Gly Ala Leu Leu Val Cys Arg
        275                 280                 285

aaa aaa cca cag aat agc tca gaa aat ttc act ttt acc ccc act tct   912
Lys Lys Pro Gln Asn Ser Ser Glu Asn Phe Thr Phe Thr Pro Thr Ser
    290                 295                 300

ttc ctc ctt tct cct tac atc acg cac aca cac aca cac aca cat gca   960
Phe Leu Leu Ser Pro Tyr Ile Thr His Thr His Thr His Thr His Ala
305                 310                 315                 320

cac aca cac gtc                                                   972
His Thr His Val
```

<210> 34
<211> 324
<212> PRT
<213> Homo sapiens

<400> 34

```
His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val Met Ala Val Phe
 1               5                  10                  15
Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe Leu Ile Tyr Met
            20                  25                  30
Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser
        35                  40                  45
Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro Lys Met Ala Ala
    50                  55                  60
Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val Gly Cys Gly Ile
65                  70                  75                  80
Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu Gly Leu Leu Leu
                85                  90                  95
Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser His Pro Leu His
```

```
            100                 105                 110
Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln Ile Thr Gly Ser
        115                 120                 125
Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln Met Val Val Val
    130                 135                 140
Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn His Phe Phe Cys
145                 150                 155                 160
Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Ile Phe Ala Cys Cys
                165                 170                 175
Val Phe Met Leu Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala
            180                 185                 190
His Ile Leu Gly Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys
        195                 200                 205
Lys Ala Leu Ala Thr Cys Ser Ser His Leu Thr Ala Phe Phe Phe Cys
    210                 215                 220
Gln Leu Pro Tyr Gln Ile Leu Ser His Gln Val Val Cys Ser Phe Tyr
225                 230                 235                 240
Trp Val Ile Leu Gly His Arg Cys Asp Lys Ser Ser Leu Gln Ser Ser
                245                 250                 255
Thr Val Ser Leu Ser Phe Ala Val Leu Asn Pro Ile Leu Tyr Gly Ser
            260                 265                 270
Val Ala Arg Ser Phe Arg Arg Arg Ala Gly Ala Leu Leu Val Cys Arg
        275                 280                 285
Lys Lys Pro Gln Asn Ser Ser Glu Asn Phe Thr Phe Thr Pro Thr Ser
    290                 295                 300

Phe Leu Leu Ser Pro Tyr Ile Thr His Thr His Thr His Thr His Ala
305                 310                 315                 320
His Thr His Val
```

<210> 35
<211> 975
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(975)

<400> 35

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ctc tgt ttc ttg cag act gag caa ttg ata act ctg tgg gtc ctc ttt   48
Leu Cys Phe Leu Gln Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe
 1               5                  10                  15

gtt ttt acc att gtt gga aac tcc gtt gtg ctt ttt tcc aca tgg agg   96
Val Phe Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg
             20                  25                  30

aga aag aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc   144
Arg Lys Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile
         35                  40                  45

aca gtg gga ttt ttg ttg gac ttt ctc atc cta ttc att atg cct ctt   192
Thr Val Gly Phe Leu Leu Asp Phe Leu Ile Leu Phe Ile Met Pro Leu
     50                  55                  60

cac ttc tct ttg gtc tat ctc ttt cac tat gag agc tca cct gat ttt   240
His Phe Ser Leu Val Tyr Leu Phe His Tyr Glu Ser Ser Pro Asp Phe
 65                  70                  75                  80

tgg tgc tta caa agc tac ttt ttt tgt gtt gtg ctg ctc tac gcc tct   288
```

```
Trp Cys Leu Gln Ser Tyr Phe Phe Cys Val Val Leu Leu Tyr Ala Ser
                 85                  90                  95

acc tac gtc ctg gtg tcc ctc agc ata gac aga tac cat gcc atc gtc   336
Thr Tyr Val Leu Val Ser Leu Ser Ile Asp Arg Tyr His Ala Ile Val
            100                 105                 110

tac ccc atg aag ttc ctt caa gga gaa aag caa gcc agg gtc ctc att   384
Tyr Pro Met Lys Phe Leu Gln Gly Glu Lys Gln Ala Arg Val Leu Ile
        115                 120                 125

gtg atc gcc tgg agc ctg tct ttt ctg ttc tcc att ccc acc ctg atc   432
Val Ile Ala Trp Ser Leu Ser Phe Leu Phe Ser Ile Pro Thr Leu Ile
    130                 135                 140

ata ttt ggg aag agg aca ctg tcc aac ggt gaa gtg cag tgc tgg gcc   480
Ile Phe Gly Lys Arg Thr Leu Ser Asn Gly Glu Val Gln Cys Trp Ala
145                 150                 155                 160

ctg tgg cct gac gac tcc tac tgg acc cca tac atg acc atc gtg gcc   528
Leu Trp Pro Asp Asp Ser Tyr Trp Thr Pro Tyr Met Thr Ile Val Ala
                165                 170                 175

ttc ctg gtg tac ttc atc cct ctg aca atc atc agc atc atg tat ggc   576
Phe Leu Val Tyr Phe Ile Pro Leu Thr Ile Ile Ser Ile Met Tyr Gly
            180                 185                 190

att gtg atc cga act att tgg att aaa agc aaa acc tac gaa aca gca   624
Ile Val Ile Arg Thr Ile Trp Ile Lys Ser Lys Thr Tyr Glu Thr Ala
        195                 200                 205

aaa atc aag gct atc aag tat agc atc atc atc att ctt gcc ttc atc   672
Lys Ile Lys Ala Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile
    210                 215                 220

tgc tgt tgg agt cca tac ttc ctg ttt gac att ttg gac aat ttc aac   720
Cys Cys Trp Ser Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn
225                 230                 235                 240

ctc ctt cca gac acc cag gag cgt ttc tat gcc tct gtg atc att cag   768
Leu Leu Pro Asp Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln
                245                 250                 255

aac ctg cca gca ttg aat agt gcc atc aac ccc ctc atc tac tac tct   816
Asn Leu Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Tyr Ser
            260                 265                 270

gtt tct caa aaa aac aaa aga aag aga aaa aga aga agt agg agg aag   864
Val Ser Gln Lys Asn Lys Arg Lys Arg Lys Arg Arg Ser Arg Arg Lys
        275                 280                 285

aag aag gaa aaa gaa aga aga aga agg aag aag aga agg aga agg aag   912
Lys Lys Glu Lys Glu Arg Arg Arg Arg Lys Lys Arg Arg Arg Arg Lys
    290                 295                 300

aag aaa gaa gga aga aga gga gga gaa gga aga gga aag aag gaa gaa   960
Lys Lys Glu Gly Arg Arg Gly Gly Glu Gly Arg Gly Lys Lys Glu Glu
305                 310                 315                 320

gag agg agg aag gaa                                             975
Glu Arg Arg Lys Glu
```

325

<210> 36
<211> 325
<212> PRT
<213> Homo sapiens

<400> 36
Leu Cys Phe Leu Gln Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe
1 5 10 15
Val Phe Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg
20 25 30
Arg Lys Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile
35 40 45
Thr Val Gly Phe Leu Leu Asp Phe Leu Ile Leu Phe Ile Met Pro Leu
50 55 60
His Phe Ser Leu Val Tyr Leu Phe His Tyr Glu Ser Ser Pro Asp Phe
65 70 75 80
Trp Cys Leu Gln Ser Tyr Phe Phe Cys Val Val Leu Leu Tyr Ala Ser
85 90 95
Thr Tyr Val Leu Val Ser Leu Ser Ile Asp Arg Tyr His Ala Ile Val
100 105 110

Tyr Pro Met Lys Phe Leu Gln Gly Glu Lys Gln Ala Arg Val Leu Ile
115 120 125
Val Ile Ala Trp Ser Leu Ser Phe Leu Phe Ser Ile Pro Thr Leu Ile
130 135 140
Ile Phe Gly Lys Arg Thr Leu Ser Asn Gly Glu Val Gln Cys Trp Ala
145 150 155 160
Leu Trp Pro Asp Asp Ser Tyr Trp Thr Pro Tyr Met Thr Ile Val Ala
165 170 175
Phe Leu Val Tyr Phe Ile Pro Leu Thr Ile Ile Ser Ile Met Tyr Gly
180 185 190
Ile Val Ile Arg Thr Ile Trp Ile Lys Ser Lys Thr Tyr Glu Thr Ala
195 200 205
Lys Ile Lys Ala Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile
210 215 220
Cys Cys Trp Ser Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn
225 230 235 240
Leu Leu Pro Asp Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln
245 250 255
Asn Leu Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Tyr Ser
260 265 270
Val Ser Gln Lys Asn Lys Arg Lys Arg Lys Arg Arg Ser Arg Arg Lys
275 280 285
Lys Lys Glu Lys Glu Arg Arg Arg Arg Lys Lys Arg Arg Arg Arg Lys
290 295 300
Lys Lys Glu Gly Arg Arg Gly Gly Glu Gly Arg Gly Lys Lys Glu Glu
305 310 315 320
Glu Arg Arg Lys Glu
325

<210> 37
<211> 969
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(969)

<400> 37

```
aac ctg gag ctg tgg aaa ata ttt tct gct gtg ttt ctt gtc atg tat   48
Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met Tyr
 1               5                  10                  15

gta gcc aca gtg ctg gaa aat cta ctt att gtg gta act att atc aca   96
Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile Thr
            20                  25                  30

agt cag agt ctg agg tca cct atg tat ttt ttt ctt acc ttc ttg tcc   144
Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu Ser
        35                  40                  45

ctt ttg gat gtc atg ttc tca tct gtc gtt gcc ccc aag gtg att gta   192
Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile Val
    50                  55                  60

gac acc ctc tcc aag agc act acc atc tct ctc aaa ggc tgc ctc acc   240
Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu Thr
65                  70                  75                  80


cag ctg ttt gtg gag cat ttc ttt ggt ggt gtg ggg atc atc ctc ctc   288
Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu Leu
                85                  90                  95

act gtg atg gcc tat gac cgc tac gtg gcc atc tgt aag ccc ctg cac   336
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
            100                 105                 110

tac acg atc atc atg agt cca cgg gtg tgc tgc cta atg gta gga ggg   384
Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly Gly
        115                 120                 125

gct tgg gtg ggg gga ttt atg cac gca atg ata caa ctt ctc ttc atg   432
Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe Met
    130                 135                 140

tat caa ata ccc ttc tgt ggt cct aat atc ata gat cac ttt ata tgt   480
Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile Cys
145                 150                 155                 160

gat ttg ttt cag ttg ttg aca ctt gcc tgc acg gac acc cac atc ctg   528
Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile Leu
                165                 170                 175

ggc ctc tta gtt acc ctc aac agt ggg atg atg tgt gtg gcc atc ttt   576
Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile Phe
            180                 185                 190

ctt atc tta att gcg tcc tac acg gtc atc cta tgc tcc ctg aag tct   624
Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys Ser
        195                 200                 205

tac agc tct aaa ggg cgg cac aaa gcc ctc tct acc tgc agc tcc cac   672
Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser His
    210                 215                 220

ctc acg gtg gtt gta ttg ttc ttt gtc ccc tgt att ttc ttg tac atg   720
Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr Met
225                 230                 235                 240
```

```
agg cct gtg gtc act cac ccc ata gac aag gca atg gct gtg tca gac   768
Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser Asp
                245                 250                 255

tca atc atc aca ccc atg tta aat ccc ttg atc tat aca ctg agg aat   816
Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
            260                 265                 270

gca gag gac ata aga gag ata ctg agg ctg atg ttt cgt gcc ccc ttt   864
Ala Glu Asp Ile Arg Glu Ile Leu Arg Leu Met Phe Arg Ala Pro Phe
        275                 280                 285

tgt cct tta ttt tat ttt att ttt cca ggc tgg tct caa aat cct gag   912
Cys Pro Leu Phe Tyr Phe Ile Phe Pro Gly Trp Ser Gln Asn Pro Glu
    290                 295                 300

ctc agg tcg ccc tcc tcg gcc tcc caa agt tct gga gtt aca ggt gtg   960
Leu Arg Ser Pro Ser Ser Ala Ser Gln Ser Ser Gly Val Thr Gly Val
305                 310                 315                 320

agc cac tgc                                                      969
Ser His Cys
```

<210> 38
<211> 323
<212> PRT
<213> Homo sapiens

<400> 38

```
Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met Tyr
 1               5                  10                  15
Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile Thr
            20                  25                  30
Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu Ser
        35                  40                  45
Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile Val
    50                  55                  60
Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu Thr
65                  70                  75                  80
Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu Leu
                85                  90                  95
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
            100                 105                 110
Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly Gly
        115                 120                 125
Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe Met
    130                 135                 140
Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile Cys
145                 150                 155                 160
Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile Leu
                165                 170                 175
Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile Phe
            180                 185                 190
Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys Ser
        195                 200                 205
Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser His
    210                 215                 220
Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr Met
225                 230                 235                 240
Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser Asp
                245                 250                 255
```

```
Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
            260                 265                 270
Ala Glu Asp Ile Arg Glu Ile Leu Arg Leu Met Phe Arg Ala Pro Phe
        275                 280                 285
Cys Pro Leu Phe Tyr Phe Ile Phe Pro Gly Trp Ser Gln Asn Pro Glu
    290                 295                 300
Leu Arg Ser Pro Ser Ser Ala Ser Gln Ser Ser Gly Val Thr Gly Val
305                 310                 315                 320
Ser His Cys
```

<210> 39
<211> 924
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(924)

<400> 39

```
gtg cac acg gcc tac ctg gtg ctg agc tcc ctg gcc atg ttc acc tgc   48
Val His Thr Ala Tyr Leu Val Leu Ser Ser Leu Ala Met Phe Thr Cys
 1               5                  10                  15

ctg tgc ggg atg gca ggc aac agc atg gtg atc tgg ctg ctg ggc ttt   96
Leu Cys Gly Met Ala Gly Asn Ser Met Val Ile Trp Leu Leu Gly Phe
            20                  25                  30

cga atg cac agg aac ccc ttc tgc atc tat atc ctc aac ctg gcg gca   144
Arg Met His Arg Asn Pro Phe Cys Ile Tyr Ile Leu Asn Leu Ala Ala
        35                  40                  45

gcc gac ctc ctc ttc ctc ttc agc atg gct tcc acg ctc agc ctg gaa   192
Ala Asp Leu Leu Phe Leu Phe Ser Met Ala Ser Thr Leu Ser Leu Glu
    50                  55                  60

acc cag ccc ctg gtc aat acc act gac aag gtc cac gag ctg atg aag   240
Thr Gln Pro Leu Val Asn Thr Thr Asp Lys Val His Glu Leu Met Lys
65                  70                  75                  80

aga ctg atg tac ttt gcc tac aca gtg ggc ctg agc ctg ctg acg gcc   288
Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly Leu Ser Leu Leu Thr Ala
                85                  90                  95

atc agc acc cag cgc tgt ctc tct gtc ctc ttc cct atc tgg ttc aag   336
Ile Ser Thr Gln Arg Cys Leu Ser Val Leu Phe Pro Ile Trp Phe Lys
            100                 105                 110

tgt cac cgg ccc agg cac ctg tca gcc tgg gtg tgt ggc ctg ctg tgg   384
Cys His Arg Pro Arg His Leu Ser Ala Trp Val Cys Gly Leu Leu Trp
        115                 120                 125

aca ctc tgt ctc ctg atg aac ggg ttg acc tct tcc ttc tgc agc aag   432
Thr Leu Cys Leu Leu Met Asn Gly Leu Thr Ser Ser Phe Cys Ser Lys
    130                 135                 140

ttc ttg aaa ttc aat gaa gat cgg tgc ttc agg gtg gac atg gtc cag   480
Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe Arg Val Asp Met Val Gln
145                 150                 155                 160

gcc gcc ctc atc atg ggg gtc tta acc cca gtg atg act ctg tcc agc   528
```

```
Ala Ala Leu Ile Met Gly Val Leu Thr Pro Val Met Thr Leu Ser Ser
                165                 170                 175

ctg acc ctc ttt gtc tgg gtg cgg agg agc tcc cag cag tgg cgg cgg   576
Leu Thr Leu Phe Val Trp Val Arg Arg Ser Ser Gln Gln Trp Arg Arg
            180                 185                 190

cag ccc aca cgg ctg ttc gtg gtg gtc ctg gcc tct gtc ctg gtg ttc   624
Gln Pro Thr Arg Leu Phe Val Val Val Leu Ala Ser Val Leu Val Phe
        195                 200                 205

ctc atc tgt tcc ctg cct ctg agc atc tac tgg ttt gtg ctc tac tgg   672
Leu Ile Cys Ser Leu Pro Leu Ser Ile Tyr Trp Phe Val Leu Tyr Trp
    210                 215                 220

ttg agc ctg ccg ccc gag atg cag gtc ctg tgc ttc agc ttg tca cgc   720
Leu Ser Leu Pro Pro Glu Met Gln Val Leu Cys Phe Ser Leu Ser Arg
225                 230                 235                 240


ctc tcc tcg tcc gta agc agc agc gcc aac ccc gtc atc tac ttc ctg   768
Leu Ser Ser Ser Val Ser Ser Ser Ala Asn Pro Val Ile Tyr Phe Leu
                245                 250                 255

gtg ggc agc cgg agg agc cac agg ctg ccc acc aga cag ggg cgg tgc   816
Val Gly Ser Arg Arg Ser His Arg Leu Pro Thr Arg Gln Gly Arg Cys
            260                 265                 270

ctc aca ctg tca acc cga ttc cgt gag aac tct atc acg aga aca gca   864
Leu Thr Leu Ser Thr Arg Phe Arg Glu Asn Ser Ile Thr Arg Thr Ala
        275                 280                 285

cca cgg ggg aaa tcc acc ccc agg atc caa tca cct tcc acc agg cca   912
Pro Arg Gly Lys Ser Thr Pro Arg Ile Gln Ser Pro Ser Thr Arg Pro
    290                 295                 300

cac atc cta caa                                                  924
His Ile Leu Gln
305
```

<210> 40
<211> 308
<212> PRT
<213> Homo sapiens

<400> 40

```
Val His Thr Ala Tyr Leu Val Leu Ser Ser Leu Ala Met Phe Thr Cys
 1               5                  10                  15
Leu Cys Gly Met Ala Gly Asn Ser Met Val Ile Trp Leu Leu Gly Phe
            20                  25                  30
Arg Met His Arg Asn Pro Phe Cys Ile Tyr Ile Leu Asn Leu Ala Ala
        35                  40                  45
Ala Asp Leu Leu Phe Leu Phe Ser Met Ala Ser Thr Leu Ser Leu Glu
    50                  55                  60
Thr Gln Pro Leu Val Asn Thr Thr Asp Lys Val His Glu Leu Met Lys
65                  70                  75                  80
Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly Leu Ser Leu Leu Thr Ala
                85                  90                  95
Ile Ser Thr Gln Arg Cys Leu Ser Val Leu Phe Pro Ile Trp Phe Lys
            100                 105                 110
Cys His Arg Pro Arg His Leu Ser Ala Trp Val Cys Gly Leu Leu Trp
```

```
        115                 120                 125
Thr Leu Cys Leu Leu Met Asn Gly Leu Thr Ser Ser Phe Cys Ser Lys
    130                 135                 140
Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe Arg Val Asp Met Val Gln
145                 150                 155                 160
Ala Ala Leu Ile Met Gly Val Leu Thr Pro Val Met Thr Leu Ser Ser
                165                 170                 175
Leu Thr Leu Phe Val Trp Val Arg Arg Ser Ser Gln Gln Trp Arg Arg
            180                 185                 190
Gln Pro Thr Arg Leu Phe Val Val Val Leu Ala Ser Val Leu Val Phe
        195                 200                 205
Leu Ile Cys Ser Leu Pro Leu Ser Ile Tyr Trp Phe Val Leu Tyr Trp
    210                 215                 220
Leu Ser Leu Pro Pro Glu Met Gln Val Leu Cys Phe Ser Leu Ser Arg
225                 230                 235                 240
Leu Ser Ser Ser Val Ser Ser Ser Ala Asn Pro Val Ile Tyr Phe Leu
                245                 250                 255
Val Gly Ser Arg Arg Ser His Arg Leu Pro Thr Arg Gln Gly Arg Cys
            260                 265                 270

Leu Thr Leu Ser Thr Arg Phe Arg Glu Asn Ser Ile Thr Arg Thr Ala
        275                 280                 285
Pro Arg Gly Lys Ser Thr Pro Arg Ile Gln Ser Pro Ser Thr Arg Pro
    290                 295                 300
His Ile Leu Gln
305


<210> 41
<211> 951
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(951)

<400> 41
ccg tgt gtg gct ggc gtc atc cct gtc atc tac tac agt gtc ctg ctg   48
Pro Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu
 1               5                  10                  15

ggc ttg ggg ctg cct ggt gac ctc ctg acc gca gtg gcc ctg gcg cgc   96
Gly Leu Gly Leu Pro Gly Asp Leu Leu Thr Ala Val Ala Leu Ala Arg
            20                  25                  30

ctt gcc acc agg acc agg agg ccc tcc tac tac tac ctt ctg gcg ctc   144
Leu Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu
        35                  40                  45

aca gcc tcg gat atc atc atc cag gtg gtc atc gtg ttc gcg ggc ttc   192
Thr Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe
    50                  55                  60

ctc ctg cag gga gca gtg ctg gcc cgc cag gtg ccc cag gct gtg gtg   240
Leu Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val
65                  70                  75                  80

cgc acg gcc aac atc ctg gag ttt gct gcc aac cac gcc tca gtc tgg   288
Arg Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp
                85                  90                  95

atc gcc atc ctg ctc acg gtt gac cgc tac act gcc ctg tgc cac ccc   336
```

```
Ile Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro
            100                 105                 110

ctg cac cat cgg gcc gcc tcg tcc cca ggc cgg acc cgc cgg gcc att   384
Leu His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile
        115                 120                 125

gct gct gtc ctg agt gct gcc ctg ttg acc ggc atc ccc ttc tac tgg   432
Ala Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp
    130                 135                 140

tgg ctg gac atg tgg aga gac acc gac tca ccc aga aca ctg gac gag   480
Trp Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu
145                 150                 155                 160

gtc ctc aag tgg gct cac tgt ctc act gtc tat ttc atc cct tgt ggc   528
Val Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly
                165                 170                 175

gtg ttc ctg gtc acc aac tcg gcc atc atc cac cgg cta cgg agg agg   576
Val Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg
            180                 185                 190

ggc cgg agt ggg ctg cag ccc cgg gtg ggc aag agc aca gcc atc ctc   624
Gly Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu
        195                 200                 205

ctg ggc atc acc aca ctg ttc acc ctc ctg tgg gcg ccc cgg gtc ttc   672
Leu Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe
    210                 215                 220

gtc atg ctc tac cac atg tac gtg gcc cct gtc cac cgg gac tgg agg   720
Val Met Leu Tyr His Met Tyr Val Ala Pro Val His Arg Asp Trp Arg
225                 230                 235                 240

gtc cac ctg gcc ttg gat gtg gcc aat atg gtg gcc atg ctc cac acg   768
Val His Leu Ala Leu Asp Val Ala Asn Met Val Ala Met Leu His Thr
                245                 250                 255

gca gcc aac ttc ggc ctc tac tgc ttt gtc agc aag act ttc cgg gcc   816
Ala Ala Asn Phe Gly Leu Tyr Cys Phe Val Ser Lys Thr Phe Arg Ala
            260                 265                 270

act ttt tgc tct tgt tgc cca agc tgt agt gca atg ggg cga tct cag   864
Thr Phe Cys Ser Cys Cys Pro Ser Cys Ser Ala Met Gly Arg Ser Gln
        275                 280                 285

ctc act gca acc tcc tcc tcc cgg gtt caa gca gtt ctc ctg cct cag   912
Leu Thr Ala Thr Ser Ser Ser Arg Val Gln Ala Val Leu Leu Pro Gln
    290                 295                 300

cct ccc gag gag ctg gga cta cag gcg cgt gcc acc aca               951
Pro Pro Glu Glu Leu Gly Leu Gln Ala Arg Ala Thr Thr
305                 310                 315
```

<210> 42
<211> 317
<212> PRT
<213> Homo sapiens

<400> 42
Pro Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu

```
 1               5                  10                  15
Gly Leu Gly Leu Pro Gly Asp Leu Leu Thr Ala Val Ala Leu Ala Arg
            20                  25                  30
Leu Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu
        35                  40                  45
Thr Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe
    50                  55                  60
Leu Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val
65                  70                  75                  80
Arg Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp
                85                  90                  95
Ile Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro
            100                 105                 110
Leu His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile
        115                 120                 125
Ala Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp
    130                 135                 140

Trp Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu
145                 150                 155                 160
Val Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly
                165                 170                 175
Val Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg
            180                 185                 190
Gly Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu
        195                 200                 205
Leu Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe
    210                 215                 220
Val Met Leu Tyr His Met Tyr Val Ala Pro Val His Arg Asp Trp Arg
225                 230                 235                 240
Val His Leu Ala Leu Asp Val Ala Asn Met Val Ala Met Leu His Thr
                245                 250                 255
Ala Ala Asn Phe Gly Leu Tyr Cys Phe Val Ser Lys Thr Phe Arg Ala
            260                 265                 270
Thr Phe Cys Ser Cys Cys Pro Ser Cys Ser Ala Met Gly Arg Ser Gln
        275                 280                 285
Leu Thr Ala Thr Ser Ser Ser Arg Val Gln Ala Val Leu Leu Pro Gln
    290                 295                 300
Pro Pro Glu Glu Leu Gly Leu Gln Ala Arg Ala Thr Thr
305                 310                 315


<210> 43
<211> 957
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(957)

<400> 43
gac cca gaa ctg aag tta atc cct ttc agc ctg ttc ctg tcc atg tac   48
Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu Ser Met Tyr
 1               5                  10                  15

ctg gtc acc atc ctg ggg aac ctg ctc att ctc ctg gct gtc atc tct   96
Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala Val Ile Ser
            20                  25                  30

gac tcc cac ctc cac acc ccc atg tac ttc ctt ctc ttt aat ctc tcc   144
Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe Asn Leu Ser
        35                  40                  45
```

```
ttt act gac atc tgt tta acc aca acc aca gtc cca aag atc cta gtg   192
Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys Ile Leu Val
     50                  55                  60

aac atc caa gct cag aat cag agt atc act tac aca ggc tgc ctc acc   240
Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly Cys Leu Thr
 65                  70                  75                  80

cag atc tgt ctt gtc ttg gtt ttt gct ggc ttg gaa agt tgc ttt ctt   288
Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser Cys Phe Leu
                85                  90                  95

gca gtc atg gcc tac gac cgc tat gtg gcc att tgc cac cca ctg agg   336
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
            100                 105                 110

tac aca gtc ctc atg aat gtc cat ttc tgg ggc ttg ctg att ctt ctc   384
Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu Ile Leu Leu
        115                 120                 125

tcc atg ttc atg agc act atg gat gcc ctg gtt cag agt ctg atg gta   432
Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser Leu Met Val
    130                 135                 140

ttg cag ctg tcc ttc tgc aaa aac gtt gaa atc cct ttg ttc ttc tgt   480
Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu Phe Phe Cys
145                 150                 155                 160

gaa ctc gcc tgt tct gac acc ctc atc aac aac atc ctc ata tat ttt   528
Glu Leu Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe
                165                 170                 175

gca agt agt gta ttt ggt gca att cct ctc tct gga ata att ttc tct   576
Ala Ser Ser Val Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser
            180                 185                 190

tat tct caa ata gtc acc tct gtt ctg aga atg cca tca gca aga gga   624
Tyr Ser Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly
        195                 200                 205

aag tat aaa gcg ttt tcc acc tgt ggc tgt cac ctc tct gtt ttt tcc   672
Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser
    210                 215                 220

ttg ttc tat ggg aca gct ttt ggg gtg tac att agt tct gct gtt gct   720
Leu Phe Tyr Gly Thr Ala Phe Gly Val Tyr Ile Ser Ser Ala Val Ala
225                 230                 235                 240

gag tct tcc cga att act gct gtg gct tca gtg atg tac act gtg gtc   768
Glu Ser Ser Arg Ile Thr Ala Val Ala Ser Val Met Tyr Thr Val Val
                245                 250                 255

cct caa atg atg aac ccc ttc atc tac agc ctg aga aat aag gag atg   816
Pro Gln Met Met Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Met
            260                 265                 270

aag aaa gct ttg agg aaa ctt att gaa tgc ctg act ctt tgt ttt gtt   864
Lys Lys Ala Leu Arg Lys Leu Ile Glu Cys Leu Thr Leu Cys Phe Val
        275                 280                 285

ttg ttt ttt tct ctg aga tgg agt ctt tct ctg tct ccc agg ctg gag   912
Leu Phe Phe Ser Leu Arg Trp Ser Leu Ser Leu Ser Pro Arg Leu Glu
```

```
    290                 295                 300

tgc aat ggc acg acc tcg gct cac tgc aac ttc cgc ctc cgg gtt       957
Cys Asn Gly Thr Thr Ser Ala His Cys Asn Phe Arg Leu Arg Val
305                 310                 315



<210> 44
<211> 319
<212> PRT
<213> Homo sapiens

<400> 44
Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu Ser Met Tyr
 1               5                  10                  15
Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala Val Ile Ser
            20                  25                  30
Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe Asn Leu Ser
        35                  40                  45
Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys Ile Leu Val
    50                  55                  60
Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly Cys Leu Thr
65                  70                  75                  80
Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser Cys Phe Leu
                85                  90                  95
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
            100                 105                 110
Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu Ile Leu Leu
        115                 120                 125
Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser Leu Met Val
    130                 135                 140
Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu Phe Phe Cys
145                 150                 155                 160
Glu Leu Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe
                165                 170                 175
Ala Ser Ser Val Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser
            180                 185                 190
Tyr Ser Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly
        195                 200                 205
Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser
    210                 215                 220
Leu Phe Tyr Gly Thr Ala Phe Gly Val Tyr Ile Ser Ser Ala Val Ala
225                 230                 235                 240
Glu Ser Ser Arg Ile Thr Ala Val Ala Ser Val Met Tyr Thr Val Val
                245                 250                 255
Pro Gln Met Met Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Met
            260                 265                 270
Lys Lys Ala Leu Arg Lys Leu Ile Glu Cys Leu Thr Leu Cys Phe Val
        275                 280                 285
Leu Phe Phe Ser Leu Arg Trp Ser Leu Ser Leu Ser Pro Arg Leu Glu
    290                 295                 300
Cys Asn Gly Thr Thr Ser Ala His Cys Asn Phe Arg Leu Arg Val
305                 310                 315



<210> 45
<211> 984
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
```

<222> (1)...(984)

<400> 45

```
gcc act gaa ttc cag gtt ctt ctc ttc ctt ctc ttc ctc ctc ctc tac   48
Ala Thr Glu Phe Gln Val Leu Leu Phe Leu Leu Phe Leu Leu Leu Tyr
 1               5                  10                  15

ttg atg atc ctc tgt ggc aac aca gcc atc atc tgg gtg gtg tgc aca   96
Leu Met Ile Leu Cys Gly Asn Thr Ala Ile Ile Trp Val Val Cys Thr
            20                  25                  30

cac agc acc ctc cgc acc ccg atg tat ttc ttc ctg tcc aac ctg tct   144
His Ser Thr Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser
        35                  40                  45

ttc ctg gaa ctc tgc tac acc acc gtg gta gta ccc ttg atg ctt tcc   192
Phe Leu Glu Leu Cys Tyr Thr Thr Val Val Val Pro Leu Met Leu Ser
    50                  55                  60

aac att ttg ggg gcc cag aag ccc att tcg ttg gct gga tgt ggg gcc   240
Asn Ile Leu Gly Ala Gln Lys Pro Ile Ser Leu Ala Gly Cys Gly Ala
65                  70                  75                  80

caa atg ttc ttc ttt gtc acc ctc ggc agc acg gac tgt ttc ctc ttg   288
Gln Met Phe Phe Phe Val Thr Leu Gly Ser Thr Asp Cys Phe Leu Leu
                85                  90                  95

gcg atc atg gcc tat gac cgc tat gtg gct atc tgc cac ccg ctg cac   336
Ala Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
            100                 105                 110

tac acc ctc atc atg acc cgc gag ctg tgc acg cag atg ctg ggt ggg   384
Tyr Thr Leu Ile Met Thr Arg Glu Leu Cys Thr Gln Met Leu Gly Gly
        115                 120                 125

gcc ctg ggc ctg gcc ctc ttc ccc tcc ctg cag ctc acc gcc tta atc   432
Ala Leu Gly Leu Ala Leu Phe Pro Ser Leu Gln Leu Thr Ala Leu Ile
    130                 135                 140

ttc acc ctg ccc ttt tgc ggc cac cac cag gaa atc aac cac ttc ctc   480
Phe Thr Leu Pro Phe Cys Gly His His Gln Glu Ile Asn His Phe Leu
145                 150                 155                 160

tgc gat gtg cct ccc gtc ctg cgc ctg gcc tgc gct gac atc cgc gtg   528
Cys Asp Val Pro Pro Val Leu Arg Leu Ala Cys Ala Asp Ile Arg Val
                165                 170                 175

cac cag gct gtc ctc tat gtc gtg agc atc ctc gtg ctg acc atc ccc   576
His Gln Ala Val Leu Tyr Val Val Ser Ile Leu Val Leu Thr Ile Pro
            180                 185                 190

ttc ctg ctc atc tgc gtc tcc tac gtg ttc atc acc tgt gcc atc ctg   624
Phe Leu Leu Ile Cys Val Ser Tyr Val Phe Ile Thr Cys Ala Ile Leu
        195                 200                 205

agc atc cgt tct gcc gag ggc cgc cgc cgg gcc ttc tcc acc tgc tcc   672
Ser Ile Arg Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser
    210                 215                 220

ttc cac ctc acc gtg gtc ctg ctg cac ttt cct ccc ctg cag gtt cac   720
Phe His Leu Thr Val Val Leu Leu His Phe Pro Pro Leu Gln Val His
225                 230                 235                 240
```

```
cac ttc ttt aaa aat tct gct cct ttc aaa acc ctg ctc att ccc ttc   768
His Phe Phe Lys Asn Ser Ala Pro Phe Lys Thr Leu Leu Ile Pro Phe
                245                 250                 255

atc cag cca ttt ggg tat gtg aat gtc atc ccc atg ttg aat ccc ctc   816
Ile Gln Pro Phe Gly Tyr Val Asn Val Ile Pro Met Leu Asn Pro Leu
            260                 265                 270

atc tac agc ctg agg aac aag gaa gtg aag gag gcc ctg aga aaa att   864
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile
        275                 280                 285



ctc aat aga gcc aag aca cag gtg aca cag aca cat aga gag act ggt   912
Leu Asn Arg Ala Lys Thr Gln Val Thr Gln Thr His Arg Glu Thr Gly
    290                 295                 300

agt cac ata cac agg cag aca gat ggg tgc agg cct agg cag aca ggc   960
Ser His Ile His Arg Gln Thr Asp Gly Cys Arg Pro Arg Gln Thr Gly
305                 310                 315                 320

aga tat ctg cat aga cag aca gaa                                  984
Arg Tyr Leu His Arg Gln Thr Glu
                325
```

<210> 46
<211> 328
<212> PRT
<213> Homo sapiens

<400> 46

```
Ala Thr Glu Phe Gln Val Leu Leu Phe Leu Leu Phe Leu Leu Leu Tyr
 1                5                  10                  15
Leu Met Ile Leu Cys Gly Asn Thr Ala Ile Ile Trp Val Val Cys Thr
            20                  25                  30
His Ser Thr Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser
        35                  40                  45
Phe Leu Glu Leu Cys Tyr Thr Thr Val Val Val Pro Leu Met Leu Ser
    50                  55                  60
Asn Ile Leu Gly Ala Gln Lys Pro Ile Ser Leu Ala Gly Cys Gly Ala
65                  70                  75                  80
Gln Met Phe Phe Phe Val Thr Leu Gly Ser Thr Asp Cys Phe Leu Leu
                85                  90                  95
Ala Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
            100                 105                 110
Tyr Thr Leu Ile Met Thr Arg Glu Leu Cys Thr Gln Met Leu Gly Gly
        115                 120                 125
Ala Leu Gly Leu Ala Leu Phe Pro Ser Leu Gln Leu Thr Ala Leu Ile
    130                 135                 140
Phe Thr Leu Pro Phe Cys Gly His His Gln Glu Ile Asn His Phe Leu
145                 150                 155                 160
Cys Asp Val Pro Pro Val Leu Arg Leu Ala Cys Ala Asp Ile Arg Val
                165                 170                 175
His Gln Ala Val Leu Tyr Val Val Ser Ile Leu Val Leu Thr Ile Pro
            180                 185                 190
Phe Leu Leu Ile Cys Val Ser Tyr Val Phe Ile Thr Cys Ala Ile Leu
        195                 200                 205
Ser Ile Arg Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser
    210                 215                 220
Phe His Leu Thr Val Val Leu Leu His Phe Pro Pro Leu Gln Val His
225                 230                 235                 240
```

```
His Phe Phe Lys Asn Ser Ala Pro Phe Lys Thr Leu Leu Ile Pro Phe
                245                 250                 255
Ile Gln Pro Phe Gly Tyr Val Asn Val Ile Pro Met Leu Asn Pro Leu
            260                 265                 270
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile
        275                 280                 285
Leu Asn Arg Ala Lys Thr Gln Val Thr Gln Thr His Arg Glu Thr Gly
    290                 295                 300
Ser His Ile His Arg Gln Thr Asp Gly Cys Arg Pro Arg Gln Thr Gly
305                 310                 315                 320
Arg Tyr Leu His Arg Gln Thr Glu
                325
```

<210> 47
<211> 939
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(939)

<400> 47

```
gac cct cag atg gag atc atc ttc ttc gtg gtc ttc ctc ata gtt tac   48
Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu Ile Val Tyr
 1               5                  10                  15

ctg gtt aat gta gtg ggg aat att ggt atg att atc ctg att aca aca   96
Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu Ile Thr Thr
            20                  25                  30

gac act cag ctt cac aca ccc atg tat ttt ttc ctc tgc aac ctc tcc   144
Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser
        35                  40                  45

ttt gtt gac ctg ggc tac tcc tca gcc att gcc ccc agg atg ctg gct   192
Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg Met Leu Ala
    50                  55                  60

gac ttc cta aca aat cac aaa gtt atc tcc ttc tcc agc tgt gcc acc   240
Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser Cys Ala Thr
65                  70                  75                  80

cag ttt gct ttt ttt gta ggt ttt gtg gat gct gag tgc tat gtc ctg   288
Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys Tyr Val Leu
                85                  90                  95

gca gcc atg gcc tat ggt cgt ttt gtg gcc att tgt cga ccc ctc cac   336
Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg Pro Leu His
            100                 105                 110

tat agc acc ttc atg tcc aag cag gtc tgc ttg gct ctc atg ctg ggc   384
Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu Met Leu Gly
        115                 120                 125

tct tac ctg gct ggt cta gtg agt tta gta gcc cac act acc ctc acc   432
Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr Thr Leu Thr
    130                 135                 140

ttc agc ctg agt tac tgt ggt tgc tgc ata tat tta aag gaa aga gca   480
Phe Ser Leu Ser Tyr Cys Gly Cys Cys Ile Tyr Leu Lys Glu Arg Ala
145                 150                 155                 160
```

```
gga cat aga aaa tta aat tat agt atc ttt ttt atc ctt ttt tct tta   528
Gly His Arg Lys Leu Asn Tyr Ser Ile Phe Phe Ile Leu Phe Ser Leu
                165                 170                 175

ttt ttc tcc ctc atc ata atc ctc atc tcc tac atc ttc att ctc att   576
Phe Phe Ser Leu Ile Ile Ile Leu Ile Ser Tyr Ile Phe Ile Leu Ile
            180                 185                 190

gcc atc ctg agg atg cgt tct gct gaa agt agg cgc aaa gcg ttc tcc   624
Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg Arg Lys Ala Phe Ser
        195                 200                 205

acc tgc ggg tcc cac ctg gtg gca gtg act gtg ttt tat gga acc ctg   672
Thr Cys Gly Ser His Leu Val Ala Val Thr Val Phe Tyr Gly Thr Leu
    210                 215                 220

ttc tgc atg tac gtt aga cct ccc acg gac agg tca gtg gaa cag tcc   720
Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg Ser Val Glu Gln Ser
225                 230                 235                 240

aaa gtc att gct gtt ttc tac act ttt gta agc cct atg ttg aac ccc   768
Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro
                245                 250                 255

atc atc tat agt ttg agg aac aag gat gtg aaa caa gct ttt tgg aaa   816
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys
            260                 265                 270

ctg atc aga aga aac aaa agc atg gcc tgt ggc agg gtg gga aag aca   864
Leu Ile Arg Arg Asn Lys Ser Met Ala Cys Gly Arg Val Gly Lys Thr
        275                 280                 285

aaa tgt tca gag agg cca gag aaa gac cca tcc att tgc agc gac agt   912
Lys Cys Ser Glu Arg Pro Glu Lys Asp Pro Ser Ile Cys Ser Asp Ser
    290                 295                 300

gaa att gtg gct gct gtt gtg aag gaa                              939
Glu Ile Val Ala Ala Val Val Lys Glu
305                 310
```

<210> 48
<211> 313
<212> PRT
<213> Homo sapiens

<400> 48

```
Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu Ile Val Tyr
 1               5                  10                  15
Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu Ile Thr Thr
            20                  25                  30
Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser
        35                  40                  45
Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg Met Leu Ala
    50                  55                  60
Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser Cys Ala Thr
65                  70                  75                  80
Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys Tyr Val Leu
                85                  90                  95
Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg Pro Leu His
            100                 105                 110
Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu Met Leu Gly
```

```
        115                 120                 125
Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr Thr Leu Thr
    130                 135                 140
Phe Ser Leu Ser Tyr Cys Gly Cys Cys Ile Tyr Leu Lys Glu Arg Ala
145                 150                 155                 160
Gly His Arg Lys Leu Asn Tyr Ser Ile Phe Phe Ile Leu Phe Ser Leu
                165                 170                 175
Phe Phe Ser Leu Ile Ile Ile Leu Ile Ser Tyr Ile Phe Ile Leu Ile
            180                 185                 190
Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg Arg Lys Ala Phe Ser
        195                 200                 205

Thr Cys Gly Ser His Leu Val Ala Val Thr Val Phe Tyr Gly Thr Leu
    210                 215                 220
Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg Ser Val Glu Gln Ser
225                 230                 235                 240
Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro
                245                 250                 255
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys
            260                 265                 270
Leu Ile Arg Arg Asn Lys Ser Met Ala Cys Gly Arg Val Gly Lys Thr
        275                 280                 285
Lys Cys Ser Glu Arg Pro Glu Lys Asp Pro Ser Ile Cys Ser Asp Ser
    290                 295                 300
Glu Ile Val Ala Ala Val Val Lys Glu
305                 310
```

<210> 49
<211> 942
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(942)

<400> 49

```
aac tca gag gta cag aga gtt ctc ttt gtg gtc ttt ttg ctg atc tat   48
Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile Tyr
 1               5                  10                  15

gtg gtc acg gtt tgt ggc aac atg ctc att gtg gtc act atc acc tcc   96
Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr Ser
             20                  25                  30

agc ccc acg ctg gct tcc cct gtg tat ttt ttc ctg gcc aac cta tcc   144
Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu Ser
         35                  40                  45

ttt att gac acc ttt tat tct tct tct atg gct cct aaa ctc att gct   192
Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile Ala
     50                  55                  60

gac tca ttg tat gag ggg aga acc atc tct tat gag tgc tgc atg gct   240
Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met Ala
 65                  70                  75                  80

cag ctc ttt gga gct cat ttt ttg gga ggt gtt gag atc att ctg ctc   288
Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu Leu
                 85                  90                  95

aca gtg atg gct tat gac cgc tat gtg gcc atc tgt aag ccc ctg cac   336
```

```
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
            100                 105                 110

aat act acc atc atg acc agg cat ctc tgt gcc atg ctt gta ggg gtg   384
Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly Val
        115                 120                 125

gct tgg ctt ggg ggc ttc ctg cat tca ttg gtt cag ctc ctc ctg gtc   432
Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu Val
    130                 135                 140

ctt tgg ttg ccc ttc tgt ggg ccc aat gtg atc aat cac ttt gcc ttt   480
Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala Phe
145                 150                 155                 160

gcc tgc acc aat acg tat gtc att ggt ctg ctg gtg gtt gcc aac agt   528
Ala Cys Thr Asn Thr Tyr Val Ile Gly Leu Leu Val Val Ala Asn Ser
                165                 170                 175

ggt tta atc tgc ctg ttg aac ttc ctc atg ctg gct gcc tcc tac att   576
Gly Leu Ile Cys Leu Leu Asn Phe Leu Met Leu Ala Ala Ser Tyr Ile
            180                 185                 190

gtc atc ctg tac tcc ttg agg tcc cac agt gca gat ggg aga tgc aaa   624
Val Ile Leu Tyr Ser Leu Arg Ser His Ser Ala Asp Gly Arg Cys Lys
        195                 200                 205

gcc ctc tcc acc tgt gga gcc cac ttc att gtt gtt gcc ttg ttc ttt   672
Ala Leu Ser Thr Cys Gly Ala His Phe Ile Val Val Ala Leu Phe Phe
    210                 215                 220

gtg ccc tgt ata ttt act tat gtg cat cca ttt tct act tta cct ata   720
Val Pro Cys Ile Phe Thr Tyr Val His Pro Phe Ser Thr Leu Pro Ile
225                 230                 235                 240

gac aaa aat atg gca tta ttt tat ggt att ctg aca cct atg ttg aat   768
Asp Lys Asn Met Ala Leu Phe Tyr Gly Ile Leu Thr Pro Met Leu Asn
                245                 250                 255

cca ctc att tat acc ctg aga aat gaa gag gta aaa aat gcc atg aga   816
Pro Leu Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Asn Ala Met Arg
            260                 265                 270

aag ctc ttt aca tgg cag gcc aac att cag att cag gaa ata cag aga   864
Lys Leu Phe Thr Trp Gln Ala Asn Ile Gln Ile Gln Glu Ile Gln Arg
        275                 280                 285

atg cca caa aga tac tcc tca aga aga gca act cca aga cac ata aat   912
Met Pro Gln Arg Tyr Ser Ser Arg Arg Ala Thr Pro Arg His Ile Asn
    290                 295                 300

gtc aga ttc acc aaa gtt gaa atg aag gaa                           942
Val Arg Phe Thr Lys Val Glu Met Lys Glu
305                 310
```

<210> 50
<211> 314
<212> PRT
<213> Homo sapiens

<400> 50
Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile Tyr

```
 1               5                  10                  15
Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr Ser
            20                  25                  30
Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu Ser
        35                  40                  45
Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile Ala
    50                  55                  60
Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met Ala
65                  70                  75                  80

Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu Leu
                85                  90                  95
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
            100                 105                 110
Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly Val
        115                 120                 125
Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu Val
    130                 135                 140
Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala Phe
145                 150                 155                 160
Ala Cys Thr Asn Thr Tyr Val Ile Gly Leu Leu Val Val Ala Asn Ser
                165                 170                 175
Gly Leu Ile Cys Leu Leu Asn Phe Leu Met Leu Ala Ala Ser Tyr Ile
            180                 185                 190
Val Ile Leu Tyr Ser Leu Arg Ser His Ser Ala Asp Gly Arg Cys Lys
        195                 200                 205
Ala Leu Ser Thr Cys Gly Ala His Phe Ile Val Val Ala Leu Phe Phe
    210                 215                 220
Val Pro Cys Ile Phe Thr Tyr Val His Pro Phe Ser Thr Leu Pro Ile
225                 230                 235                 240
Asp Lys Asn Met Ala Leu Phe Tyr Gly Ile Leu Thr Pro Met Leu Asn
                245                 250                 255
Pro Leu Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Asn Ala Met Arg
            260                 265                 270
Lys Leu Phe Thr Trp Gln Ala Asn Ile Gln Ile Gln Glu Ile Gln Arg
        275                 280                 285
Met Pro Gln Arg Tyr Ser Ser Arg Arg Ala Thr Pro Arg His Ile Asn
    290                 295                 300
Val Arg Phe Thr Lys Val Glu Met Lys Glu
305                 310
```

<210> 51
<211> 972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(972)

<400> 51

```
gac atg gaa tca tct ttc tca ttt gga gtg atc ctt gct gtc ctg gcc   48
Asp Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala
 1               5                  10                  15

tcc ctc atc att gct act aac aca cta gtg gct gtg gct gtg ctg ctg   96
Ser Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu
             20                  25                  30

ttg atc cac aag aat gat ggt gtc agt ctc tgc ttc acc ttg aat ctg   144
Leu Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu
         35                  40                  45
```

```
gct gtg gct gac acc ttg att ggt gtg gcc atc tct ggc cta ctc aca   192
Ala Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr
     50                  55                  60

gac cag ctc tcc agc cct tct cgg ccc aca cag aag acc ctg tgc agc   240
Asp Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser
 65                  70                  75                  80

ctg cgg atg gca ttt gtc act tcc tcc gca gct gcc tct gtc ctc acg   288
Leu Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr
                 85                  90                  95

gtc atg ctg atc acc ttt gac agg tac ctt gcc atc aag cag ccc ttc   336
Val Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe
            100                 105                 110

cgc tac ttg aag atc atg agt ggg ttc gtg gcc ggg gcc tgc att gcc   384
Arg Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala
        115                 120                 125

ggg ctg tgg tta gtg tct tac ctc att ggc ttc ctc cca ctc gga atc   432
Gly Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile
    130                 135                 140

ccc atg ttc cag cag act gcc tac aaa ggg cag tgc agc ttc ttt gct   480
Pro Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala
145                 150                 155                 160

gta ttt cac cct cac ttc gtg ctg acc ctc tcc tgc gtt ggc ttc ttc   528
Val Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe
                165                 170                 175

cca gcc atg ctc ctc ttt gtc ttc ttc tac tgc gac atg ctc aag att   576
Pro Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile
            180                 185                 190

gcc tcc atg cac agc cag cag att cga aag atg gaa cat gca gga gcc   624
Ala Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala
        195                 200                 205

atg gct gga gct ctc cgt act gtg tct gtt ctc att ggg agc ttt gct   672
Met Ala Gly Ala Leu Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala
    210                 215                 220

cta tcc tgg acc ccc ttc ctt atc act ggc att gtg cag gtg gcc tgc   720
Leu Ser Trp Thr Pro Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys
225                 230                 235                 240

cag gag tgt cac ctc tac cta gtg ctg gaa cgg tac ctg tgg ctg ctc   768
Gln Glu Cys His Leu Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu
                245                 250                 255

ggc gtg ggc aac tcc ctg ctc aac cca ctc atc tat gcc tat tgg cag   816
Gly Val Gly Asn Ser Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln
            260                 265                 270

aag gag ttc cgt aac att ctg ctc ttc tgc ctc aca tgt gtc tct att   864
Lys Glu Phe Arg Asn Ile Leu Leu Phe Cys Leu Thr Cys Val Ser Ile
        275                 280                 285

acc tct ttg aga aag aag ctc ttt cgt tgt att cac cat gtg gct aac   912
Thr Ser Leu Arg Lys Lys Leu Phe Arg Cys Ile His His Val Ala Asn
```

```
    290                 295                 300

ttt ata tgt ata cat atg cat aca cac aca cac aca cac aca cac aca   960
Phe Ile Cys Ile His Met His Thr His Thr His Thr His Thr His Thr
305                 310                 315                 320

cac aca cac aca                                                   972
His Thr His Thr
```

<210> 52
<211> 324
<212> PRT
<213> Homo sapiens

<400> 52

```
Asp Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala
 1               5                  10                  15
Ser Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu
            20                  25                  30
Leu Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu
        35                  40                  45
Ala Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr
    50                  55                  60
Asp Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser
65                  70                  75                  80
Leu Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr
                85                  90                  95
Val Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe
            100                 105                 110
Arg Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala
        115                 120                 125
Gly Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile
    130                 135                 140
Pro Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala
145                 150                 155                 160
Val Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe
                165                 170                 175
Pro Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile
            180                 185                 190
Ala Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala
        195                 200                 205
Met Ala Gly Ala Leu Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala
    210                 215                 220
Leu Ser Trp Thr Pro Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys
225                 230                 235                 240
Gln Glu Cys His Leu Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu
                245                 250                 255
Gly Val Gly Asn Ser Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln
            260                 265                 270
Lys Glu Phe Arg Asn Ile Leu Leu Phe Cys Leu Thr Cys Val Ser Ile
        275                 280                 285
Thr Ser Leu Arg Lys Lys Leu Phe Arg Cys Ile His His Val Ala Asn
    290                 295                 300
Phe Ile Cys Ile His Met His Thr His Thr His Thr His Thr His Thr
305                 310                 315                 320
His Thr His Thr
```

<210> 53
<211> 987

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(987)

<400> 53

```
tcc cag gac tgg aga acc atc atc ccg gct ctc ttg gtg gct gtc tgc   48
Ser Gln Asp Trp Arg Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys
 1               5                  10                  15

ctg gtg ggc ttc gtg gga aac ctg tgt gtg att ggc atc ctc ctt cac   96
Leu Val Gly Phe Val Gly Asn Leu Cys Val Ile Gly Ile Leu Leu His
            20                  25                  30

aat gct tgg aaa gga aag cca tcc atg atc cac tcc ctg att ctg aat   144
Asn Ala Trp Lys Gly Lys Pro Ser Met Ile His Ser Leu Ile Leu Asn
        35                  40                  45

ctc agc ctg gct gat ctc tcc ctc ctg ctg ttt tct gca cct atc cga   192
Leu Ser Leu Ala Asp Leu Ser Leu Leu Leu Phe Ser Ala Pro Ile Arg
    50                  55                  60

gct acg gcg tac tcc aaa agt gtt tgg gat cta ggc tgg ttt gtc tgc   240
Ala Thr Ala Tyr Ser Lys Ser Val Trp Asp Leu Gly Trp Phe Val Cys
65                  70                  75                  80

aag tcc tct gac tgg ttt atc cac aca tgc atg gca gcc aag agc ctg   288
Lys Ser Ser Asp Trp Phe Ile His Thr Cys Met Ala Ala Lys Ser Leu
                85                  90                  95

aca atc gtt gtg gtg gcc aaa gta tgc ttc atg tat gca agt gac cca   336
Thr Ile Val Val Val Ala Lys Val Cys Phe Met Tyr Ala Ser Asp Pro
            100                 105                 110

gcc aag caa gtg agt atc cac aac tac acc atc tgg tca gtg ctg gtg   384
Ala Lys Gln Val Ser Ile His Asn Tyr Thr Ile Trp Ser Val Leu Val
        115                 120                 125

gcc atc tgg act gtg gct agc ctg tta ccc ctg ccg gaa tgg ttc ttt   432
Ala Ile Trp Thr Val Ala Ser Leu Leu Pro Leu Pro Glu Trp Phe Phe
    130                 135                 140

agc acc atc agg cat cat gaa ggt gtg gaa atg tgc ctc gtg gat gta   480
Ser Thr Ile Arg His His Glu Gly Val Glu Met Cys Leu Val Asp Val
145                 150                 155                 160

cca gct gtg gct gaa gag ttt atg tcg atg ttt ggt aag ctc tac cca   528
Pro Ala Val Ala Glu Glu Phe Met Ser Met Phe Gly Lys Leu Tyr Pro
                165                 170                 175

ctc ctg gca ttt ggc ctt cca tta ttt ttt gcc agc ttt tat ttc tgg   576
Leu Leu Ala Phe Gly Leu Pro Leu Phe Phe Ala Ser Phe Tyr Phe Trp
            180                 185                 190

aga gct tat gac caa tgt aaa aaa cga gga act aag act caa aat ctt   624
Arg Ala Tyr Asp Gln Cys Lys Lys Arg Gly Thr Lys Thr Gln Asn Leu
        195                 200                 205

aga aac cag ata cgc tca aag caa gtc aca gtg atg ctg ctg agc att   672
Arg Asn Gln Ile Arg Ser Lys Gln Val Thr Val Met Leu Leu Ser Ile
    210                 215                 220
```

```
gcc atc atc tct gct ctc ttg tgg ctc ccc gaa tgg gta gct tgg ctg   720
Ala Ile Ile Ser Ala Leu Leu Trp Leu Pro Glu Trp Val Ala Trp Leu
225                 230                 235                 240

tgg gta tgg cat ctg aag gct gca ggc ccg gcc cca cca caa ggt ttc   768
Trp Val Trp His Leu Lys Ala Ala Gly Pro Ala Pro Pro Gln Gly Phe
                245                 250                 255

ata gcc ctg tct caa gtc ttg atg ttt tcc atc tct tca gca aat cct   816
Ile Ala Leu Ser Gln Val Leu Met Phe Ser Ile Ser Ser Ala Asn Pro
            260                 265                 270

ctc att ttt ctt gtg atg tcg gaa gag ttc agg gaa ggc ttg aaa gat   864
Leu Ile Phe Leu Val Met Ser Glu Glu Phe Arg Glu Gly Leu Lys Asp
        275                 280                 285

tcc atc tta aga atc cac ttt gtt tgc tca tcc atg aga agc agt tac   912
Ser Ile Leu Arg Ile His Phe Val Cys Ser Ser Met Arg Ser Ser Tyr
    290                 295                 300

tca tct gtt aaa gtt ttc tta tgc gat agc agc aat tca ggc aca tca   960
Ser Ser Val Lys Val Phe Leu Cys Asp Ser Ser Asn Ser Gly Thr Ser
305                 310                 315                 320

tca gac tcc act tct aat gcc agg tct                              987
Ser Asp Ser Thr Ser Asn Ala Arg Ser
                325
```

<210> 54
<211> 329
<212> PRT
<213> Homo sapiens

<400> 54

```
Ser Gln Asp Trp Arg Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys
 1               5                  10                  15
Leu Val Gly Phe Val Gly Asn Leu Cys Val Ile Gly Ile Leu Leu His
            20                  25                  30
Asn Ala Trp Lys Gly Lys Pro Ser Met Ile His Ser Leu Ile Leu Asn
        35                  40                  45
Leu Ser Leu Ala Asp Leu Ser Leu Leu Leu Phe Ser Ala Pro Ile Arg
    50                  55                  60
Ala Thr Ala Tyr Ser Lys Ser Val Trp Asp Leu Gly Trp Phe Val Cys
65                  70                  75                  80
Lys Ser Ser Asp Trp Phe Ile His Thr Cys Met Ala Ala Lys Ser Leu
                85                  90                  95
Thr Ile Val Val Val Ala Lys Val Cys Phe Met Tyr Ala Ser Asp Pro
            100                 105                 110
Ala Lys Gln Val Ser Ile His Asn Tyr Thr Ile Trp Ser Val Leu Val
        115                 120                 125
Ala Ile Trp Thr Val Ala Ser Leu Leu Pro Leu Pro Glu Trp Phe Phe
    130                 135                 140
Ser Thr Ile Arg His His Glu Gly Val Glu Met Cys Leu Val Asp Val
145                 150                 155                 160
Pro Ala Val Ala Glu Glu Phe Met Ser Met Phe Gly Lys Leu Tyr Pro
                165                 170                 175
Leu Leu Ala Phe Gly Leu Pro Leu Phe Phe Ala Ser Phe Tyr Phe Trp
            180                 185                 190
Arg Ala Tyr Asp Gln Cys Lys Lys Arg Gly Thr Lys Thr Gln Asn Leu
```

```
        195                 200                 205
Arg Asn Gln Ile Arg Ser Lys Gln Val Thr Val Met Leu Leu Ser Ile
    210                 215                 220
Ala Ile Ile Ser Ala Leu Leu Trp Leu Pro Glu Trp Val Ala Trp Leu
225                 230                 235                 240

Trp Val Trp His Leu Lys Ala Ala Gly Pro Ala Pro Pro Gln Gly Phe
                245                 250                 255
Ile Ala Leu Ser Gln Val Leu Met Phe Ser Ile Ser Ser Ala Asn Pro
            260                 265                 270
Leu Ile Phe Leu Val Met Ser Glu Glu Phe Arg Glu Gly Leu Lys Asp
        275                 280                 285
Ser Ile Leu Arg Ile His Phe Val Cys Ser Ser Met Arg Ser Ser Tyr
    290                 295                 300
Ser Ser Val Lys Val Phe Leu Cys Asp Ser Ser Asn Ser Gly Thr Ser
305                 310                 315                 320
Ser Asp Ser Thr Ser Asn Ala Arg Ser
                325


<210> 55
<211> 954
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(954)

<400> 55
tgc tac aag cag acc ctg agc ttc acg ggg ctg acg tgc atc gtt tcc   48
Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly Leu Thr Cys Ile Val Ser
 1               5                  10                  15

ctt gtc gcg ctg aca gga aac gcg gtt gtg ctc tgg ctc ctg ggc tgc   96
Leu Val Ala Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Cys
            20                  25                  30

cgc atg cgc agg aac gct gtc tcc atc tac atc ctc aac ctg gtc gcg   144
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Val Ala
        35                  40                  45

gcc gac ttc ctc ttc ctt agc ggc cac att ata tgt tcg ccg tta cgc   192
Ala Asp Phe Leu Phe Leu Ser Gly His Ile Ile Cys Ser Pro Leu Arg
    50                  55                  60

ctc atc aat atc cgc cat ccc atc tcc aaa atc ctc agt cct gtg atg   240
Leu Ile Asn Ile Arg His Pro Ile Ser Lys Ile Leu Ser Pro Val Met
65                  70                  75                  80

acc ttt ccc tac ttt ata ggc cta agc atg ctg agc gcc atc agc acc   288
Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
                85                  90                  95

gag cgc tgc ctc atc aaa cac tgc ata tct gcc ctg tgg ccc atc tgg   336
Glu Arg Cys Leu Ile Lys His Cys Ile Ser Ala Leu Trp Pro Ile Trp
            100                 105                 110

tac cac tgc cgt cgc ccc aca cac ctg tca gca gtc ctg tgt gcc ctg   384
Tyr His Cys Arg Arg Pro Thr His Leu Ser Ala Val Leu Cys Ala Leu
        115                 120                 125

ctc tgg gcc ccg tcc ctg ctg ctt gcc ttc ctg gaa ggt tac tac tgt   432
```

```
Leu Trp Ala Pro Ser Leu Leu Leu Ala Phe Leu Glu Gly Tyr Tyr Cys
    130                 135                 140


gct ttt ctg ttt aag att ggg gac tac agt tgg ttt cag aca ttt gat   480
Ala Phe Leu Phe Lys Ile Gly Asp Tyr Ser Trp Phe Gln Thr Phe Asp
145                 150                 155                 160

ttc atc aca ggc acg tgg ctg att ttt aaa ttt gtg gtt ctc ttc tat   528
Phe Ile Thr Gly Thr Trp Leu Ile Phe Lys Phe Val Val Leu Phe Tyr
                165                 170                 175

gtt ccc ctg aaa atc atg ttc tgt tct gag att gga att aca agc gtg   576
Val Pro Leu Lys Ile Met Phe Cys Ser Glu Ile Gly Ile Thr Ser Val
            180                 185                 190

agc cac cgc gcc cag ccg aca atc tct tta acc cat atg gtt gca tca   624
Ser His Arg Ala Gln Pro Thr Ile Ser Leu Thr His Met Val Ala Ser
        195                 200                 205

tat cta gga gta atg ttg ctg ctc ttc ctt att tgc agc ctg ccc tta   672
Tyr Leu Gly Val Met Leu Leu Leu Phe Leu Ile Cys Ser Leu Pro Leu
    210                 215                 220

ggc att aag tgg ttc cta tta ttc tgg atc ctc gtg gat ttt gat atc   720
Gly Ile Lys Trp Phe Leu Leu Phe Trp Ile Leu Val Asp Phe Asp Ile
225                 230                 235                 240

ttc ctt tgt cat ttg caa cca gtt tca gat gtc ctg tcc tct ctt aac   768
Phe Leu Cys His Leu Gln Pro Val Ser Asp Val Leu Ser Ser Leu Asn
                245                 250                 255

agc agt gcc aac ccc atc att tac ttc ttc atg ggc tcc ttt agg cag   816
Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met Gly Ser Phe Arg Gln
            260                 265                 270

cgt gtt ttt tgt tgt tgt tgt tgt tgt tgc tgc tgt tgt ttt aca aaa   864
Arg Val Phe Cys Cys Cys Cys Cys Cys Cys Cys Cys Cys Phe Thr Lys
        275                 280                 285

ttc ctg tta gga ata act ttt gtg tcc agg cgc ggt ggc tca cac ctg   912
Phe Leu Leu Gly Ile Thr Phe Val Ser Arg Arg Gly Gly Ser His Leu
    290                 295                 300

cat tcc ggc cat tcc agg cat gtc ccc tcc cat tcc agg cat           954
His Ser Gly His Ser Arg His Val Pro Ser His Ser Arg His
305                 310                 315


<210> 56
<211> 318
<212> PRT
<213> Homo sapiens

<400> 56
Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly Leu Thr Cys Ile Val Ser
 1               5                  10                  15
Leu Val Ala Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Cys
            20                  25                  30
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Val Ala
        35                  40                  45
```

```
Ala Asp Phe Leu Phe Leu Ser Gly His Ile Ile Cys Ser Pro Leu Arg
    50                  55                  60
Leu Ile Asn Ile Arg His Pro Ile Ser Lys Ile Leu Ser Pro Val Met
65                  70                  75                  80
Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
                85                  90                  95
Glu Arg Cys Leu Ile Lys His Cys Ile Ser Ala Leu Trp Pro Ile Trp
            100                 105                 110
Tyr His Cys Arg Arg Pro Thr His Leu Ser Ala Val Leu Cys Ala Leu
        115                 120                 125
Leu Trp Ala Pro Ser Leu Leu Leu Ala Phe Leu Glu Gly Tyr Tyr Cys
    130                 135                 140
Ala Phe Leu Phe Lys Ile Gly Asp Tyr Ser Trp Phe Gln Thr Phe Asp
145                 150                 155                 160
Phe Ile Thr Gly Thr Trp Leu Ile Phe Lys Phe Val Val Leu Phe Tyr
                165                 170                 175
Val Pro Leu Lys Ile Met Phe Cys Ser Glu Ile Gly Ile Thr Ser Val
            180                 185                 190
Ser His Arg Ala Gln Pro Thr Ile Ser Leu Thr His Met Val Ala Ser
        195                 200                 205
Tyr Leu Gly Val Met Leu Leu Leu Phe Leu Ile Cys Ser Leu Pro Leu
    210                 215                 220
Gly Ile Lys Trp Phe Leu Leu Phe Trp Ile Leu Val Asp Phe Asp Ile
225                 230                 235                 240
Phe Leu Cys His Leu Gln Pro Val Ser Asp Val Leu Ser Ser Leu Asn
                245                 250                 255
Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met Gly Ser Phe Arg Gln
            260                 265                 270
Arg Val Phe Cys Cys Cys Cys Cys Cys Cys Cys Cys Cys Phe Thr Lys
        275                 280                 285
Phe Leu Leu Gly Ile Thr Phe Val Ser Arg Arg Gly Gly Ser His Leu
    290                 295                 300
His Ser Gly His Ser Arg His Val Pro Ser His Ser Arg His
305                 310                 315
```

<210> 57
<211> 972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(972)

<400> 57

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gag cga ctg ctc cga ctc atc tct gct ggg gtc tgt ggc ctc atc ctg   48
Glu Arg Leu Leu Arg Leu Ile Ser Ala Gly Val Cys Gly Leu Ile Leu
 1               5                  10                  15

ctg gtg ggg ctg tca gct aat ggg ctc atg ctg ctg gtg gtg ggc cgg   96
Leu Val Gly Leu Ser Ala Asn Gly Leu Met Leu Leu Val Val Gly Arg
            20                  25                  30

ggc ccg ggc tcc ccc cac ccg ctc cac tcc ctg acc cac agc ctc atg   144
Gly Pro Gly Ser Pro His Pro Leu His Ser Leu Thr His Ser Leu Met
        35                  40                  45

atg aac atc acg cca tct gac ctg ctc ttc ctg gcc tgc gtg gtg cct   192
Met Asn Ile Thr Pro Ser Asp Leu Leu Phe Leu Ala Cys Val Val Pro
    50                  55                  60

gtg ctg ctg ctg agc ttc ctg cag cac aac tgg tgg ctg ggc cct gcc   240
```

```
Val Leu Leu Leu Ser Phe Leu Gln His Asn Trp Trp Leu Gly Pro Ala
 65                  70                  75                  80

atc tgc acc att agc cag gcc acc aac aca gcc acc acg ttc tgc atc   288
Ile Cys Thr Ile Ser Gln Ala Thr Asn Thr Ala Thr Thr Phe Cys Ile
                 85                  90                  95

ttc tat agc atg gtg gcc aca gct ctc ctg cgc cat gtg gct gtg gcc   336
Phe Tyr Ser Met Val Ala Thr Ala Leu Leu Arg His Val Ala Val Ala
            100                 105                 110

cgg cct gac ctg gcc ttc cca gcc ggc tgg ggc acc ctc ttg ctg ctc   384
Arg Pro Asp Leu Ala Phe Pro Ala Gly Trp Gly Thr Leu Leu Leu Leu
        115                 120                 125

tgt ggg gcc atg tgg gcc ctg ggc ctt aca gaa tcc ctg ccc aac tgg   432
Cys Gly Ala Met Trp Ala Leu Gly Leu Thr Glu Ser Leu Pro Asn Trp
    130                 135                 140

ctg ttc cag agg gtg gca gtg gag gag gag aca gcg ggg gct ccc aag   480
Leu Phe Gln Arg Val Ala Val Glu Glu Glu Thr Ala Gly Ala Pro Lys
145                 150                 155                 160

acc cag gcc tgc ctc ttg ctc ctg agc cct gct ggg acc tcc tgc tac   528
Thr Gln Ala Cys Leu Leu Leu Leu Ser Pro Ala Gly Thr Ser Cys Tyr
                165                 170                 175

atc agc ctg ctg gga gcc ctg gcc ttc ctg cca tgc acg ctg ggg ctg   576
Ile Ser Leu Leu Gly Ala Leu Ala Phe Leu Pro Cys Thr Leu Gly Leu
            180                 185                 190

ggc tgc tct ttc agc cac gtg ggc tgg ctc ctg tgg acc cag ccc caa   624
Gly Cys Ser Phe Ser His Val Gly Trp Leu Leu Trp Thr Gln Pro Gln
        195                 200                 205

gag aac ata ggg ctc agc ctt gtg gtg ctg gtg gtt ttt gtg ctg atg   672
Glu Asn Ile Gly Leu Ser Leu Val Val Leu Val Val Phe Val Leu Met
    210                 215                 220

tgg ggg ccc tgc tcc atg ctg ggt tat gtg gca gcc atg ggc tac ctg   720
Trp Gly Pro Cys Ser Met Leu Gly Tyr Val Ala Ala Met Gly Tyr Leu
225                 230                 235                 240

cct gcc aca ccg gct gct ttt gtg gcc tcc agc ctc tgc acc atc ctg   768
Pro Ala Thr Pro Ala Ala Phe Val Ala Ser Ser Leu Cys Thr Ile Leu
                245                 250                 255

gcc tac tcc aat tgc gct gtc agc cct atc ctc tgc ttc tac ctc tcc   816
Ala Tyr Ser Asn Cys Ala Val Ser Pro Ile Leu Cys Phe Tyr Leu Ser
            260                 265                 270

cgc ccc ttc cag gca gga ctc agg gac ctc ttc tgc agg ccg atg atg   864
Arg Pro Phe Gln Ala Gly Leu Arg Asp Leu Phe Cys Arg Pro Met Met
        275                 280                 285

gcc agg cat ccc aga ggt cct ggg caa caa gag cga gac tct gtc tca   912
Ala Arg His Pro Arg Gly Pro Gly Gln Gln Glu Arg Asp Ser Val Ser
    290                 295                 300

aat aat aaa aca aaa acc aaa aca cac aca cac aca cac aca cac aca   960
Asn Asn Lys Thr Lys Thr Lys Thr His Thr His Thr His Thr His Thr
305                 310                 315                 320
```

cac aca cac aca 972
His Thr His Thr

<210> 58
<211> 324
<212> PRT
<213> Homo sapiens

<400> 58
Glu Arg Leu Leu Arg Leu Ile Ser Ala Gly Val Cys Gly Leu Ile Leu
1 5 10 15
Leu Val Gly Leu Ser Ala Asn Gly Leu Met Leu Leu Val Val Gly Arg
20 25 30
Gly Pro Gly Ser Pro His Pro Leu His Ser Leu Thr His Ser Leu Met
35 40 45
Met Asn Ile Thr Pro Ser Asp Leu Leu Phe Leu Ala Cys Val Val Pro
50 55 60
Val Leu Leu Leu Ser Phe Leu Gln His Asn Trp Trp Leu Gly Pro Ala
65 70 75 80
Ile Cys Thr Ile Ser Gln Ala Thr Asn Thr Ala Thr Thr Phe Cys Ile
85 90 95
Phe Tyr Ser Met Val Ala Thr Ala Leu Leu Arg His Val Ala Val Ala
100 105 110
Arg Pro Asp Leu Ala Phe Pro Ala Gly Trp Gly Thr Leu Leu Leu Leu
115 120 125
Cys Gly Ala Met Trp Ala Leu Gly Leu Thr Glu Ser Leu Pro Asn Trp
130 135 140
Leu Phe Gln Arg Val Ala Val Glu Glu Glu Thr Ala Gly Ala Pro Lys
145 150 155 160
Thr Gln Ala Cys Leu Leu Leu Leu Ser Pro Ala Gly Thr Ser Cys Tyr
165 170 175
Ile Ser Leu Leu Gly Ala Leu Ala Phe Leu Pro Cys Thr Leu Gly Leu
180 185 190
Gly Cys Ser Phe Ser His Val Gly Trp Leu Leu Trp Thr Gln Pro Gln
195 200 205
Glu Asn Ile Gly Leu Ser Leu Val Val Leu Val Val Phe Val Leu Met
210 215 220
Trp Gly Pro Cys Ser Met Leu Gly Tyr Val Ala Ala Met Gly Tyr Leu
225 230 235 240
Pro Ala Thr Pro Ala Ala Phe Val Ala Ser Ser Leu Cys Thr Ile Leu
245 250 255
Ala Tyr Ser Asn Cys Ala Val Ser Pro Ile Leu Cys Phe Tyr Leu Ser
260 265 270
Arg Pro Phe Gln Ala Gly Leu Arg Asp Leu Phe Cys Arg Pro Met Met
275 280 285
Ala Arg His Pro Arg Gly Pro Gly Gln Gln Glu Arg Asp Ser Val Ser
290 295 300
Asn Asn Lys Thr Lys Thr Lys Thr His Thr His Thr His Thr His Thr
305 310 315 320
His Thr His Thr

<210> 59
<211> 873
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(873)

<400> 59

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tct tta gca ctc tac aat gtc ttt cca ttt ttt ttc tgg ctt ctt ttt   48
Ser Leu Ala Leu Tyr Asn Val Phe Pro Phe Phe Phe Trp Leu Leu Phe
 1               5                  10                  15

gtg ggg gca ctg ctg ggc aac ggc gcg ctg ctg gtc gtg gtg ctg cgc   96
Val Gly Ala Leu Leu Gly Asn Gly Ala Leu Leu Val Val Val Leu Arg
            20                  25                  30

acg ccg gga ctg cgc gac gcg ctc tac ctg gcg cac ctg tgc gtc gtg   144
Thr Pro Gly Leu Arg Asp Ala Leu Tyr Leu Ala His Leu Cys Val Val
        35                  40                  45

gac ctg ctg gcg gcc gcc tcc atc atg ccg ctg ggc ctg ctg gcc gca   192
Asp Leu Leu Ala Ala Ala Ser Ile Met Pro Leu Gly Leu Leu Ala Ala
    50                  55                  60

ccg ccg ccc ggg ctg ggc cgc gtg cgc ctg ggc ccc gcg cca tgc cgc   240
Pro Pro Pro Gly Leu Gly Arg Val Arg Leu Gly Pro Ala Pro Cys Arg
65                  70                  75                  80

gcc gct cgc ttc ctc tcc gcc gct ctg ctg ccg gcc tgc acg ctc ggg   288
Ala Ala Arg Phe Leu Ser Ala Ala Leu Leu Pro Ala Cys Thr Leu Gly
                85                  90                  95

gtg gcc gca ctt ggc ctg gca cgc tac cgc ctc atc gtg cac ccg ctg   336
Val Ala Ala Leu Gly Leu Ala Arg Tyr Arg Leu Ile Val His Pro Leu
            100                 105                 110

cgg cca ggc tcg cgg ccg ccg cct gtg ctc gtg ctc acc gcc gtg tgg   384
Arg Pro Gly Ser Arg Pro Pro Pro Val Leu Val Leu Thr Ala Val Trp
        115                 120                 125

gcc gcg gcg gga ctg ctg ggc gcg ctc tcc ctg ctc ggc ccg ccg ccc   432
Ala Ala Ala Gly Leu Leu Gly Ala Leu Ser Leu Leu Gly Pro Pro Pro
    130                 135                 140

gca ccg ccc cct gct cct gct cgc tgc tcg gtc ctg gct ggg ggc ctc   480
Ala Pro Pro Pro Ala Pro Ala Arg Cys Ser Val Leu Ala Gly Gly Leu
145                 150                 155                 160

ggg ccc ttc cgg ccg ctc tgg gcc ctg ctg gcc ttc gcg ctg ccc gcc   528
Gly Pro Phe Arg Pro Leu Trp Ala Leu Leu Ala Phe Ala Leu Pro Ala
                165                 170                 175

ctc ctg ctg ctc ggc gcc tac ggc ggc atc ttc gtg gtg gcg ccg ctg   576
Leu Leu Leu Leu Gly Ala Tyr Gly Gly Ile Phe Val Val Ala Pro Leu
            180                 185                 190

gcc gtg ggc caa ttt gca gcc tgc tgg ctg cct tat ggc tgc gcg tgc   624
Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro Tyr Gly Cys Ala Cys
        195                 200                 205

ctg gcg ccc gca gcg cgg gcc gcg gaa gcc gaa gcg gct gtc acc tgg   672
Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu Ala Ala Val Thr Trp
    210                 215                 220

gtc gcc tac tcg gcc ttc gcg gct cac ccc ttc ctg tac ggg ctg ctg   720
Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe Leu Tyr Gly Leu Leu
225                 230                 235                 240
```

```
cag cgc ccc gtg cgc ttg gca ctg ggc cgc ctc tct cgc ctg agg agc   768
Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu Ser Arg Leu Arg Ser
                245                 250                 255

agc tgg gcg gtg agg acc aca tct gga tca aga ctg ctc aga ggc cct   816
Ser Trp Ala Val Arg Thr Thr Ser Gly Ser Arg Leu Leu Arg Gly Pro
            260                 265                 270

tgc agt gtg ctt gac caa acg ctg tca agt tca ggg ccc agc ctg gct   864
Cys Ser Val Leu Asp Gln Thr Leu Ser Ser Ser Gly Pro Ser Leu Ala
        275                 280                 285

ggg tcc tcc                                                       873
Gly Ser Ser
    290
```

<210> 60
<211> 291
<212> PRT
<213> Homo sapiens

<400> 60

```
Ser Leu Ala Leu Tyr Asn Val Phe Pro Phe Phe Phe Trp Leu Leu Phe
 1               5                  10                  15
Val Gly Ala Leu Leu Gly Asn Gly Ala Leu Leu Val Val Val Leu Arg
            20                  25                  30
Thr Pro Gly Leu Arg Asp Ala Leu Tyr Leu Ala His Leu Cys Val Val
        35                  40                  45
Asp Leu Leu Ala Ala Ala Ser Ile Met Pro Leu Gly Leu Leu Ala Ala
    50                  55                  60
Pro Pro Pro Gly Leu Gly Arg Val Arg Leu Gly Pro Ala Pro Cys Arg
65                  70                  75                  80
Ala Ala Arg Phe Leu Ser Ala Ala Leu Leu Pro Ala Cys Thr Leu Gly
                85                  90                  95
Val Ala Ala Leu Gly Leu Ala Arg Tyr Arg Leu Ile Val His Pro Leu
            100                 105                 110
Arg Pro Gly Ser Arg Pro Pro Pro Val Leu Val Leu Thr Ala Val Trp
        115                 120                 125
Ala Ala Ala Gly Leu Leu Gly Ala Leu Ser Leu Leu Gly Pro Pro Pro
    130                 135                 140
Ala Pro Pro Pro Ala Pro Ala Arg Cys Ser Val Leu Ala Gly Gly Leu
145                 150                 155                 160
Gly Pro Phe Arg Pro Leu Trp Ala Leu Leu Ala Phe Ala Leu Pro Ala
                165                 170                 175
Leu Leu Leu Leu Gly Ala Tyr Gly Gly Ile Phe Val Val Ala Pro Leu
            180                 185                 190
Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro Tyr Gly Cys Ala Cys
        195                 200                 205
Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu Ala Ala Val Thr Trp
    210                 215                 220
Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe Leu Tyr Gly Leu Leu
225                 230                 235                 240
Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu Ser Arg Leu Arg Ser
                245                 250                 255
Ser Trp Ala Val Arg Thr Thr Ser Gly Ser Arg Leu Leu Arg Gly Pro
            260                 265                 270
Cys Ser Val Leu Asp Gln Thr Leu Ser Ser Ser Gly Pro Ser Leu Ala
        275                 280                 285
Gly Ser Ser
    290
```

<210> 61
<211> 1326
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1326)

<400> 61

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aca cac ctt cca tca gca tcg tcc caa atc cca gct ctc gaa gag agc   48
Thr His Leu Pro Ser Ala Ser Ser Gln Ile Pro Ala Leu Glu Glu Ser
 1               5                  10                  15

tgt gag gct gtg gaa gcc cga gaa atc atg tgg ttt aag act cgt caa   96
Cys Glu Ala Val Glu Ala Arg Glu Ile Met Trp Phe Lys Thr Arg Gln
             20                  25                  30

gga cag ata gca aag cag cca tgc cct gca gga act ata ggt gta tca   144
Gly Gln Ile Ala Lys Gln Pro Cys Pro Ala Gly Thr Ile Gly Val Ser
         35                  40                  45

act tat cta tgc ctt gct cct gat gga att tgg gat ccc caa ggt cca   192
Thr Tyr Leu Cys Leu Ala Pro Asp Gly Ile Trp Asp Pro Gln Gly Pro
     50                  55                  60

gat ctc agc aac tgt tct tct cct tgg gtc aat cat ata aca cag aag   240
Asp Leu Ser Asn Cys Ser Ser Pro Trp Val Asn His Ile Thr Gln Lys
 65                  70                  75                  80

cgc tct tgc aga gcc tat gtc cag tca gag gaa aat ttc aac cct aac   288
Arg Ser Cys Arg Ala Tyr Val Gln Ser Glu Glu Asn Phe Asn Pro Asn
                 85                  90                  95

tgt tca ttt tgg agc tac tcc aag cgt aca atg aca ggt tat tgg tca   336
Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr Gly Tyr Trp Ser
            100                 105                 110

aca caa ggc tgt cgg ctc ctg aca aca aat aag aca cat act aca tgc   384
Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr His Thr Thr Cys
        115                 120                 125

tct tgt aac cac cta aca aat ttt gca gta ctg atg gca cat gtg gaa   432
Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met Ala His Val Glu
    130                 135                 140

cac agt gat gcg gtc cat gac ctc ctt ctg gat gtg atc acg tgg gtt   480
His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr Trp Val
145                 150                 155                 160

gga att ttg ctg tcc ctt gtt tgt ctc ctg att tgc atc ttc aca ttt   528
Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe Thr Phe
                165                 170                 175

tgc ttt ttc cgg ggg ctc cag agt gac cgt aac acc atc cac aag aac   576
Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys Asn
            180                 185                 190

ctc tgc atc agt ctc ttt gta gca gag ctg ctc ttc ctg att ggg atc   624
Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile Gly Ile
        195                 200                 205

aac cga act gac caa cca att gcc tgt gct gtt ttc gct gcc ctg tta   672
```

```
Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala Val Phe Ala Ala Leu Leu
    210                 215                 220

cat ttc ttc ttc ttg gct gcc ttc acc tgg atg ttc ctg gag ggg gtg   720
His Phe Phe Phe Leu Ala Ala Phe Thr Trp Met Phe Leu Glu Gly Val
225                 230                 235                 240

cag ctt tat atc atg ctg gtg gag gtt ttt gag agt gaa cat tca cgt   768
Gln Leu Tyr Ile Met Leu Val Glu Val Phe Glu Ser Glu His Ser Arg
                245                 250                 255

agg aaa tac ttt tat ctg gtc ggc tat ggg atg cct gca ctc att gtg   816
Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly Met Pro Ala Leu Ile Val
            260                 265                 270

gct gtg tca gct gca gta gac tac agg agt tat gga aca gat aaa gta   864
Ala Val Ser Ala Ala Val Asp Tyr Arg Ser Tyr Gly Thr Asp Lys Val
        275                 280                 285

tgt tgg ctc cga ctt gac acc tac ttc att tgg agt ttt ata gga cca   912
Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile Trp Ser Phe Ile Gly Pro
    290                 295                 300

gca act ttg ata att atg ctt aat gta atc ttc ctt ggg att gct tta   960
Ala Thr Leu Ile Ile Met Leu Asn Val Ile Phe Leu Gly Ile Ala Leu
305                 310                 315                 320

tat aaa atg ttt cat cat act gct ata ctg aaa cct gaa tca ggc tgt  1008
Tyr Lys Met Phe His His Thr Ala Ile Leu Lys Pro Glu Ser Gly Cys
                325                 330                 335

ctt gat aac atc aag tca tgg gtt ata ggt gca ata gct ctt ctc tgc  1056
Leu Asp Asn Ile Lys Ser Trp Val Ile Gly Ala Ile Ala Leu Leu Cys
            340                 345                 350

cta tta gga ttg acc tgg gcc ttt gga ctc atg tat att aat gaa agc  1104
Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu Met Tyr Ile Asn Glu Ser
        355                 360                 365

aca gtc atc atg gcc tat ctc ttc acc att ttc aat tct cta cag gga  1152
Thr Val Ile Met Ala Tyr Leu Phe Thr Ile Phe Asn Ser Leu Gln Gly
    370                 375                 380

atg ttt ata ttt att ttc cat tgt gtc cta cag aag aag gta cga aaa  1200
Met Phe Ile Phe Ile Phe His Cys Val Leu Gln Lys Lys Val Arg Lys
385                 390                 395                 400

gag tat ggg aaa tgc ctg cga aca cat tgc tgt agt ggc aaa agt aca  1248
Glu Tyr Gly Lys Cys Leu Arg Thr His Cys Cys Ser Gly Lys Ser Thr
                405                 410                 415

gag agt tcc att ggt tca ggg aaa aca tct ggt tct cga act cct gga  1296
Glu Ser Ser Ile Gly Ser Gly Lys Thr Ser Gly Ser Arg Thr Pro Gly
            420                 425                 430

cgc tac tcc aca ggc tca cag gta aac aat                         1326
Arg Tyr Ser Thr Gly Ser Gln Val Asn Asn
        435                 440
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<210> 62
<211> 442
<212> PRT

<213> Homo sapiens

<400> 62

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Thr His Leu Pro Ser Ala Ser Ser Gln Ile Pro Ala Leu Glu Glu Ser
 1               5                  10                  15
Cys Glu Ala Val Glu Ala Arg Glu Ile Met Trp Phe Lys Thr Arg Gln
            20                  25                  30
Gly Gln Ile Ala Lys Gln Pro Cys Pro Ala Gly Thr Ile Gly Val Ser
        35                  40                  45
Thr Tyr Leu Cys Leu Ala Pro Asp Gly Ile Trp Asp Pro Gln Gly Pro
    50                  55                  60
Asp Leu Ser Asn Cys Ser Ser Pro Trp Val Asn His Ile Thr Gln Lys
65                  70                  75                  80
Arg Ser Cys Arg Ala Tyr Val Gln Ser Glu Glu Asn Phe Asn Pro Asn
                85                  90                  95
Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr Gly Tyr Trp Ser
            100                 105                 110
Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr His Thr Thr Cys
        115                 120                 125
Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met Ala His Val Glu
    130                 135                 140
His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr Trp Val
145                 150                 155                 160
Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe Thr Phe
                165                 170                 175
Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys Asn
            180                 185                 190
Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile Gly Ile
        195                 200                 205
Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala Val Phe Ala Ala Leu Leu
    210                 215                 220
His Phe Phe Phe Leu Ala Ala Phe Thr Trp Met Phe Leu Glu Gly Val
225                 230                 235                 240
Gln Leu Tyr Ile Met Leu Val Glu Val Phe Glu Ser Glu His Ser Arg
                245                 250                 255
Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly Met Pro Ala Leu Ile Val
            260                 265                 270
Ala Val Ser Ala Ala Val Asp Tyr Arg Ser Tyr Gly Thr Asp Lys Val
        275                 280                 285
Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile Trp Ser Phe Ile Gly Pro
    290                 295                 300
Ala Thr Leu Ile Ile Met Leu Asn Val Ile Phe Leu Gly Ile Ala Leu
305                 310                 315                 320
Tyr Lys Met Phe His His Thr Ala Ile Leu Lys Pro Glu Ser Gly Cys
                325                 330                 335
Leu Asp Asn Ile Lys Ser Trp Val Ile Gly Ala Ile Ala Leu Leu Cys
            340                 345                 350
Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu Met Tyr Ile Asn Glu Ser
        355                 360                 365
Thr Val Ile Met Ala Tyr Leu Phe Thr Ile Phe Asn Ser Leu Gln Gly
    370                 375                 380
Met Phe Ile Phe Ile Phe His Cys Val Leu Gln Lys Lys Val Arg Lys
385                 390                 395                 400
Glu Tyr Gly Lys Cys Leu Arg Thr His Cys Cys Ser Gly Lys Ser Thr
                405                 410                 415
Glu Ser Ser Ile Gly Ser Gly Lys Thr Ser Gly Ser Arg Thr Pro Gly
            420                 425                 430
Arg Tyr Ser Thr Gly Ser Gln Val Asn Asn
        435                 440
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<210> 63
<211> 1275

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1275)

<400> 63

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cac agg agg ctg aag cag gag aat cac ttg aac ccg gga ggc aga ggt   48
His Arg Arg Leu Lys Gln Glu Asn His Leu Asn Pro Gly Gly Arg Gly
 1               5                  10                  15

tgc atg ggg ctt tgg ggt ggg ggt ctt tgc tgg gtg ccc acc gcg cca   96
Cys Met Gly Leu Trp Gly Gly Gly Leu Cys Trp Val Pro Thr Ala Pro
            20                  25                  30

ggg agc tgc ggt gct ccc ccg ggc cgc ctg cgg tgc ccc gac tgg ttc   144
Gly Ser Cys Gly Ala Pro Pro Gly Arg Leu Arg Cys Pro Asp Trp Phe
        35                  40                  45

tct gcc ctg tcc tca act agc atg atg tca ggt cct tca ctc tcc ctc   192
Ser Ala Leu Ser Ser Thr Ser Met Met Ser Gly Pro Ser Leu Ser Leu
    50                  55                  60

tgc tgt cct cac gga ccc agg tgt ctg cag aca gga cac tgg agc ccc   240
Cys Cys Pro His Gly Pro Arg Cys Leu Gln Thr Gly His Trp Ser Pro
65                  70                  75                  80

agg atg cag gcc act gtc tcc gga gaa ggg gtc tgg tcg aac cac ggc   288
Arg Met Gln Ala Thr Val Ser Gly Glu Gly Val Trp Ser Asn His Gly
                85                  90                  95

tgt gcg ctc acg aga gga aac ctc acc tac tcc gtc tgc cgc tgc act   336
Cys Ala Leu Thr Arg Gly Asn Leu Thr Tyr Ser Val Cys Arg Cys Thr
            100                 105                 110

cac ctc acc aac ttt gcc atc ctc atg cag ctt gca cgc gga cac cag   384
His Leu Thr Asn Phe Ala Ile Leu Met Gln Leu Ala Arg Gly His Gln
        115                 120                 125

gtg gcg ctg tcg tct atc agc tat gtg ggc tgc tcc ctc tcc gtg ctc   432
Val Ala Leu Ser Ser Ile Ser Tyr Val Gly Cys Ser Leu Ser Val Leu
    130                 135                 140

tgc ctg gtg gcc acg ctg gtc acc ttc gcc gtg ctg tcc acc atc cgg   480
Cys Leu Val Ala Thr Leu Val Thr Phe Ala Val Leu Ser Thr Ile Arg
145                 150                 155                 160

aac cag cgc tac cac atc cac gcc aac ctg tcc ttc gcc gtg ctg gtg   528
Asn Gln Arg Tyr His Ile His Ala Asn Leu Ser Phe Ala Val Leu Val
                165                 170                 175

gcc cag gtc ctg ctg ctc att agt ttc cgc ctc gag ccg ggc acg gtg   576
Ala Gln Val Leu Leu Leu Ile Ser Phe Arg Leu Glu Pro Gly Thr Val
            180                 185                 190

agt ggg cgc agc tcc acc ccc tgc caa gtg atg gcc gtg ctc cta cac   624
Ser Gly Arg Ser Ser Thr Pro Cys Gln Val Met Ala Val Leu Leu His
        195                 200                 205

tac ttc ttc ctg agt gcc ttc gca tgg atg ctg gtg gag ggg ctg cac   672
Tyr Phe Phe Leu Ser Ala Phe Ala Trp Met Leu Val Glu Gly Leu His
    210                 215                 220
```

```
ctc tac agc atg gtg atc aag gtc ttt ggg tcg gag gac agc aag cac   720
Leu Tyr Ser Met Val Ile Lys Val Phe Gly Ser Glu Asp Ser Lys His
225                 230                 235                 240

cgt tac tac tat ggg atg gga tgg ggt ttt cct ctt ctg atc tgc atc   768
Arg Tyr Tyr Tyr Gly Met Gly Trp Gly Phe Pro Leu Leu Ile Cys Ile
                245                 250                 255

att tca ctg tca ttt gcc atg gac agt tac gga aca agc aac aat tgc   816
Ile Ser Leu Ser Phe Ala Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys
            260                 265                 270

tgg ctg tcg ttg gcg agt ggc gcc atc tgg gcc ttt gta gcc cct gcc   864
Trp Leu Ser Leu Ala Ser Gly Ala Ile Trp Ala Phe Val Ala Pro Ala
        275                 280                 285

ctg ttt gtc atc gtg gta cct aat ttt gta ttt tta gta gag acg ggt   912
Leu Phe Val Ile Val Val Pro Asn Phe Val Phe Leu Val Glu Thr Gly
    290                 295                 300

cca gtt ttg ctt act gga cta gcg agc caa gac cct tct gtg cgc tcc   960
Pro Val Leu Leu Thr Gly Leu Ala Ser Gln Asp Pro Ser Val Arg Ser
305                 310                 315                 320

acc cag ttg acg gcc aag gca gcg gcc gtg ctg ctg ccc atc ctg ggt   1008
Thr Gln Leu Thr Ala Lys Ala Ala Ala Val Leu Leu Pro Ile Leu Gly
                325                 330                 335

acc tcg tgg gtc ttt ggc gtg ctt gct gtc aac ggt tgt gct gtg gtt   1056
Thr Ser Trp Val Phe Gly Val Leu Ala Val Asn Gly Cys Ala Val Val
            340                 345                 350

ttc cag tac atg ttt gcc acg ctc aac tcc ctg cag gga ctg ttc ata   1104
Phe Gln Tyr Met Phe Ala Thr Leu Asn Ser Leu Gln Gly Leu Phe Ile
        355                 360                 365

ttc ctc ttt cat tgt ctc ctg aat tca gag gta cag ggg ctg gag gag   1152
Phe Leu Phe His Cys Leu Leu Asn Ser Glu Val Gln Gly Leu Glu Glu
    370                 375                 380

ctg cag aag aaa tgg tgg ggc ggt gac cct gag tta ggc atc agc agg   1200
Leu Gln Lys Lys Trp Trp Gly Gly Asp Pro Glu Leu Gly Ile Ser Arg
385                 390                 395                 400

aag cca ctg cca tcc ggg gct gca ggg gcc ggg aag ggt gag cac agc   1248
Lys Pro Leu Pro Ser Gly Ala Ala Gly Ala Gly Lys Gly Glu His Ser
                405                 410                 415

cag ggc ctg ggt ggc aag tcc agg gca                               1275
Gln Gly Leu Gly Gly Lys Ser Arg Ala
            420                 425
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<210> 64
<211> 425
<212> PRT
<213> Homo sapiens

<400> 64

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His Arg Arg Leu Lys Gln Glu Asn His Leu Asn Pro Gly Gly Arg Gly
 1               5                  10                  15
Cys Met Gly Leu Trp Gly Gly Gly Leu Cys Trp Val Pro Thr Ala Pro
```

```
            20                  25                  30
Gly Ser Cys Gly Ala Pro Pro Gly Arg Leu Arg Cys Pro Asp Trp Phe
        35                  40                  45
Ser Ala Leu Ser Ser Thr Ser Met Met Ser Gly Pro Ser Leu Ser Leu
    50                  55                  60
Cys Cys Pro His Gly Pro Arg Cys Leu Gln Thr Gly His Trp Ser Pro
65                  70                  75                  80
Arg Met Gln Ala Thr Val Ser Gly Glu Gly Val Trp Ser Asn His Gly
                85                  90                  95
Cys Ala Leu Thr Arg Gly Asn Leu Thr Tyr Ser Val Cys Arg Cys Thr
            100                 105                 110
His Leu Thr Asn Phe Ala Ile Leu Met Gln Leu Ala Arg Gly His Gln
        115                 120                 125
Val Ala Leu Ser Ser Ile Ser Tyr Val Gly Cys Ser Leu Ser Val Leu
    130                 135                 140
Cys Leu Val Ala Thr Leu Val Thr Phe Ala Val Leu Ser Thr Ile Arg
145                 150                 155                 160
Asn Gln Arg Tyr His Ile His Ala Asn Leu Ser Phe Ala Val Leu Val
                165                 170                 175
Ala Gln Val Leu Leu Leu Ile Ser Phe Arg Leu Glu Pro Gly Thr Val
            180                 185                 190
Ser Gly Arg Ser Ser Thr Pro Cys Gln Val Met Ala Val Leu Leu His
        195                 200                 205
Tyr Phe Phe Leu Ser Ala Phe Ala Trp Met Leu Val Glu Gly Leu His
    210                 215                 220
Leu Tyr Ser Met Val Ile Lys Val Phe Gly Ser Glu Asp Ser Lys His
225                 230                 235                 240
Arg Tyr Tyr Tyr Gly Met Gly Trp Gly Phe Pro Leu Leu Ile Cys Ile
                245                 250                 255
Ile Ser Leu Ser Phe Ala Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys
            260                 265                 270
Trp Leu Ser Leu Ala Ser Gly Ala Ile Trp Ala Phe Val Ala Pro Ala
        275                 280                 285
Leu Phe Val Ile Val Val Pro Asn Phe Val Phe Leu Val Glu Thr Gly
    290                 295                 300
Pro Val Leu Leu Thr Gly Leu Ala Ser Gln Asp Pro Ser Val Arg Ser
305                 310                 315                 320
Thr Gln Leu Thr Ala Lys Ala Ala Ala Val Leu Leu Pro Ile Leu Gly
                325                 330                 335
Thr Ser Trp Val Phe Gly Val Leu Ala Val Asn Gly Cys Ala Val Val
            340                 345                 350
Phe Gln Tyr Met Phe Ala Thr Leu Asn Ser Leu Gln Gly Leu Phe Ile
        355                 360                 365
Phe Leu Phe His Cys Leu Leu Asn Ser Glu Val Gln Gly Leu Glu Glu
    370                 375                 380
Leu Gln Lys Lys Trp Trp Gly Gly Asp Pro Glu Leu Gly Ile Ser Arg
385                 390                 395                 400
Lys Pro Leu Pro Ser Gly Ala Ala Gly Ala Gly Lys Gly Glu His Ser
                405                 410                 415
Gln Gly Leu Gly Gly Lys Ser Arg Ala
            420                 425
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<210> 65
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1275)

<400> 65

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tat tat cag gaa caa ttg gca cag aaa gac cct ttg acg tac tta aat   48
Tyr Tyr Gln Glu Gln Leu Ala Gln Lys Asp Pro Leu Thr Tyr Leu Asn
 1               5                  10                  15

gat aat tgc ttt att ctt cct gat att ttc act tgt aga ttc acc tgc   96
Asp Asn Cys Phe Ile Leu Pro Asp Ile Phe Thr Cys Arg Phe Thr Cys
            20                  25                  30

cca tgg ggc caa tct tgt agt ctt tgc cca tac cta tgt cct gaa tgg   144
Pro Trp Gly Gln Ser Cys Ser Leu Cys Pro Tyr Leu Cys Pro Glu Trp
        35                  40                  45

ttc cag ttg ttt cct tct gct cag gtt atc aga agc tgc aca aag tgg   192
Phe Gln Leu Phe Pro Ser Ala Gln Val Ile Arg Ser Cys Thr Lys Trp
    50                  55                  60

tct ggt act tgg gac act ttt ttt gga gga tgg aac acg tca gga tgt   240
Ser Gly Thr Trp Asp Thr Phe Phe Gly Gly Trp Asn Thr Ser Gly Cys
65                  70                  75                  80

gtt gca cac aga gat tca gat gca agt gag aca gtc tgc ctg tgt aac   288
Val Ala His Arg Asp Ser Asp Ala Ser Glu Thr Val Cys Leu Cys Asn
                85                  90                  95

cac ttc aca cac ttt gga gtt ctg atg tta gat gca aga aac act aaa   336
His Phe Thr His Phe Gly Val Leu Met Leu Asp Ala Arg Asn Thr Lys
            100                 105                 110

gtc ctc act ttc atc agc tat att ggg tgt gga ata tct gct att ttt   384
Val Leu Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile Phe
        115                 120                 125

tca gca gca act ctc ctg aca tat gtt gct ttt gaa ttc ctt ttt tca   432
Ser Ala Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Phe Leu Phe Ser
    130                 135                 140

ttt ttt agg aaa ttg cga agg gat tat ccc tcc aaa atc ttg atg aac   480
Phe Phe Arg Lys Leu Arg Arg Asp Tyr Pro Ser Lys Ile Leu Met Asn
145                 150                 155                 160

ctg agc aca gcc ctg ctg ttc ctg aat ctc ctc ttc ctc cta gat ggc   528
Leu Ser Thr Ala Leu Leu Phe Leu Asn Leu Leu Phe Leu Leu Asp Gly
                165                 170                 175

tgg atc acc tcc ttc aat gtg gat gga ctt tgc att gct gtt gca gtc   576
Trp Ile Thr Ser Phe Asn Val Asp Gly Leu Cys Ile Ala Val Ala Val
            180                 185                 190

ctg ttg cat ttc ttc ctt ctg gca acc ttt acc tgg atg ggg cta gaa   624
Leu Leu His Phe Phe Leu Leu Ala Thr Phe Thr Trp Met Gly Leu Glu
        195                 200                 205

gca att cac atg tac att gct cta gtt aaa gta ttt aac act tac att   672
Ala Ile His Met Tyr Ile Ala Leu Val Lys Val Phe Asn Thr Tyr Ile
    210                 215                 220


cgc cga tac att cta aaa ttc tgc atc att ggc tgg ggt ttg cct gcc   720
Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile Gly Trp Gly Leu Pro Ala
225                 230                 235                 240

tta gtg gtg tca gtt gtt cta gcg agc aga aac aac aat gaa gtc tat   768
Leu Val Val Ser Val Val Leu Ala Ser Arg Asn Asn Asn Glu Val Tyr
```

```
                245                 250                 255

gga aaa gaa agt tat ggg aaa gaa aaa ggt gat gaa ttc tgt tgg att   816
Gly Lys Glu Ser Tyr Gly Lys Glu Lys Gly Asp Glu Phe Cys Trp Ile
            260                 265                 270

caa gat cca gtc ata ttt tat gtg acc tgt gct ggg tat ttt gga gtc   864
Gln Asp Pro Val Ile Phe Tyr Val Thr Cys Ala Gly Tyr Phe Gly Val
        275                 280                 285

atg ttt ttt ctg aac att gcc atg ttc att gtg gta atg gtg cag atc   912
Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val Gln Ile
    290                 295                 300

tgt ggg agg aat ggc aag aga agc aac cgg acc ctg aga gaa gaa gtg   960
Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu Glu Val
305                 310                 315                 320

tta agg aac ctg cgc agt gtg gtt agc ttg acc ttt ctg ttg ggc atg   1008
Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu Gly Met
                325                 330                 335

aca tgg ggt ttt gca ttc ttt gcc tgg gga ccc tta aat atc ccc ttc   1056
Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile Pro Phe
            340                 345                 350

atg tac ctc ttc tcc atc ttc aat tca tta caa ggc tta ttt ata ttc   1104
Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu Gln Gly Leu Phe Ile Phe
        355                 360                 365

atc ttc cac tgt gct atg aag gag aat gtt cag aaa cag tgg cgg cag   1152
Ile Phe His Cys Ala Met Lys Glu Asn Val Gln Lys Gln Trp Arg Gln
    370                 375                 380

cat ctc tgc tgt ggt aga ttt cgt ggc acg atc tcg gct cac tgc aag   1200
His Leu Cys Cys Gly Arg Phe Arg Gly Thr Ile Ser Ala His Cys Lys
385                 390                 395                 400

ctc cgc ctc ccc ggt tca cgc cat tct cct gcc tca gcc tcc caa gta   1248
Leu Arg Leu Pro Gly Ser Arg His Ser Pro Ala Ser Ala Ser Gln Val
                405                 410                 415

gct ggg act aca ggc acc agc cac cat                              1275
Ala Gly Thr Thr Gly Thr Ser His His
            420                 425


<210> 66
<211> 425
<212> PRT
<213> Homo sapiens

<400> 66
Tyr Tyr Gln Glu Gln Leu Ala Gln Lys Asp Pro Leu Thr Tyr Leu Asn
 1               5                  10                  15

Asp Asn Cys Phe Ile Leu Pro Asp Ile Phe Thr Cys Arg Phe Thr Cys
            20                  25                  30
Pro Trp Gly Gln Ser Cys Ser Leu Cys Pro Tyr Leu Cys Pro Glu Trp
        35                  40                  45
Phe Gln Leu Phe Pro Ser Ala Gln Val Ile Arg Ser Cys Thr Lys Trp
    50                  55                  60
Ser Gly Thr Trp Asp Thr Phe Phe Gly Gly Trp Asn Thr Ser Gly Cys
```

```
65                  70                  75                  80
Val Ala His Arg Asp Ser Asp Ala Ser Glu Thr Val Cys Leu Cys Asn
                85                  90                  95
His Phe Thr His Phe Gly Val Leu Met Leu Asp Ala Arg Asn Thr Lys
            100                 105                 110
Val Leu Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile Phe
        115                 120                 125
Ser Ala Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Phe Leu Phe Ser
    130                 135                 140
Phe Phe Arg Lys Leu Arg Arg Asp Tyr Pro Ser Lys Ile Leu Met Asn
145                 150                 155                 160
Leu Ser Thr Ala Leu Leu Phe Leu Asn Leu Leu Phe Leu Leu Asp Gly
                165                 170                 175
Trp Ile Thr Ser Phe Asn Val Asp Gly Leu Cys Ile Ala Val Ala Val
            180                 185                 190
Leu Leu His Phe Phe Leu Leu Ala Thr Phe Thr Trp Met Gly Leu Glu
        195                 200                 205
Ala Ile His Met Tyr Ile Ala Leu Val Lys Val Phe Asn Thr Tyr Ile
    210                 215                 220
Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile Gly Trp Gly Leu Pro Ala
225                 230                 235                 240
Leu Val Val Ser Val Val Leu Ala Ser Arg Asn Asn Asn Glu Val Tyr
                245                 250                 255
Gly Lys Glu Ser Tyr Gly Lys Glu Lys Gly Asp Glu Phe Cys Trp Ile
            260                 265                 270
Gln Asp Pro Val Ile Phe Tyr Val Thr Cys Ala Gly Tyr Phe Gly Val
        275                 280                 285
Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val Gln Ile
    290                 295                 300
Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu Glu Val
305                 310                 315                 320
Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu Gly Met
                325                 330                 335
Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile Pro Phe
            340                 345                 350
Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu Gln Gly Leu Phe Ile Phe
        355                 360                 365
Ile Phe His Cys Ala Met Lys Glu Asn Val Gln Lys Gln Trp Arg Gln
    370                 375                 380
His Leu Cys Cys Gly Arg Phe Arg Gly Thr Ile Ser Ala His Cys Lys
385                 390                 395                 400
Leu Arg Leu Pro Gly Ser Arg His Ser Pro Ala Ser Ala Ser Gln Val
                405                 410                 415
Ala Gly Thr Thr Gly Thr Ser His His
            420                 425
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<210> 67
<211> 2454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2454)

<400> 67

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gga cat atc ata att gga ggt ttg ttt gct att cat gaa aaa atg ttg   48
Gly His Ile Ile Ile Gly Gly Leu Phe Ala Ile His Glu Lys Met Leu
 1               5                  10                  15

tcc tca gaa gac tct ccc aga cga cca caa atc cag gag tgt gtt ggc   96
Ser Ser Glu Asp Ser Pro Arg Arg Pro Gln Ile Gln Glu Cys Val Gly
```

```
                20                  25                  30

ttt gaa ata tca gtt ttt ctt caa act ctt gcc atg ata cac agc att   144
Phe Glu Ile Ser Val Phe Leu Gln Thr Leu Ala Met Ile His Ser Ile
        35                  40                  45

gag atg atc aac aat tca aca ctc tta cct gga gtc aaa ctg ggg tat   192
Glu Met Ile Asn Asn Ser Thr Leu Leu Pro Gly Val Lys Leu Gly Tyr
    50                  55                  60

gaa atc tat gac act tgt aca gaa gtc aca gtg gca atg gca gcc act   240
Glu Ile Tyr Asp Thr Cys Thr Glu Val Thr Val Ala Met Ala Ala Thr
65                  70                  75                  80

ctg agg ttt ctt tct aaa ttc aac tgc tcc aga gaa act gtg gag ttt   288
Leu Arg Phe Leu Ser Lys Phe Asn Cys Ser Arg Glu Thr Val Glu Phe
                85                  90                  95

aag tgt gac tat tcc agc tac atg cca aga gtt aag gct gtc ata ggt   336
Lys Cys Asp Tyr Ser Ser Tyr Met Pro Arg Val Lys Ala Val Ile Gly
            100                 105                 110

tct ggg tac tca gaa ata act atg gct gtc tcc agg atg ttg aat tta   384
Ser Gly Tyr Ser Glu Ile Thr Met Ala Val Ser Arg Met Leu Asn Leu
        115                 120                 125

cag ctc atg cca cag gtg ggt tat gaa tca act gca gaa atc ctg agt   432
Gln Leu Met Pro Gln Val Gly Tyr Glu Ser Thr Ala Glu Ile Leu Ser
    130                 135                 140

gac aaa att cgc ttt cct tca ttt tta cgg act gtg ccc agt gac ttc   480
Asp Lys Ile Arg Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Phe
145                 150                 155                 160

cat caa att aaa gca atg gct cac ctg att cag aaa tct ggt tgg aac   528
His Gln Ile Lys Ala Met Ala His Leu Ile Gln Lys Ser Gly Trp Asn
                165                 170                 175

tgg att ggc atc ata acc aca gat gat gac tat gga cga ttg gct ctt   576
Trp Ile Gly Ile Ile Thr Thr Asp Asp Asp Tyr Gly Arg Leu Ala Leu
            180                 185                 190

aac act ttt ata att cag gct gaa gca aat aac gtg tgc ata gcc ttc   624
Asn Thr Phe Ile Ile Gln Ala Glu Ala Asn Asn Val Cys Ile Ala Phe
        195                 200                 205

aaa gag gtt ctt cca gcc ttt ctt tca gat aat acc att gaa gtc aga   672
Lys Glu Val Leu Pro Ala Phe Leu Ser Asp Asn Thr Ile Glu Val Arg
    210                 215                 220

atc aat cgg aca ctg aag aaa atc att tta gaa gcc cag gtt aat gtc   720
Ile Asn Arg Thr Leu Lys Lys Ile Ile Leu Glu Ala Gln Val Asn Val
225                 230                 235                 240


att gtg gta ttt ctg agg caa ttc cat gtt ttt gat ctc ttc aat aaa   768
Ile Val Val Phe Leu Arg Gln Phe His Val Phe Asp Leu Phe Asn Lys
                245                 250                 255

gcc att gaa atg aat ata aat aag atg tgg att gct agt gat aat tgg   816
Ala Ile Glu Met Asn Ile Asn Lys Met Trp Ile Ala Ser Asp Asn Trp
            260                 265                 270
```

```
tca act gcc acc aag att acc acc att cct aat gtt aaa aag att ggc   864
Ser Thr Ala Thr Lys Ile Thr Thr Ile Pro Asn Val Lys Lys Ile Gly
        275                 280                 285

aaa gtt gta ggg ttt gcc ttt aga aga ggg aat ata tcc tct ttc cat   912
Lys Val Val Gly Phe Ala Phe Arg Arg Gly Asn Ile Ser Ser Phe His
    290                 295                 300

tcc ttt ctt caa aat ctg cac ttg ctt ccc agt gac agt cac aaa ctc   960
Ser Phe Leu Gln Asn Leu His Leu Leu Pro Ser Asp Ser His Lys Leu
305                 310                 315                 320

tta cat gaa tat gcc atg cat tta tct gcc tgc gca tat gtc aag gac   1008
Leu His Glu Tyr Ala Met His Leu Ser Ala Cys Ala Tyr Val Lys Asp
                325                 330                 335

act gat ttg agt caa tgc ata ttc aat cat tct caa agg act ttg gcc   1056
Thr Asp Leu Ser Gln Cys Ile Phe Asn His Ser Gln Arg Thr Leu Ala
            340                 345                 350

tac aag gct aac aag gct ata gaa agg aac ttc gtc atg aga aat gac   1104
Tyr Lys Ala Asn Lys Ala Ile Glu Arg Asn Phe Val Met Arg Asn Asp
        355                 360                 365

ttc ctc tgg gac tat gct gag cca gga ctc att cat agt att cag ctt   1152
Phe Leu Trp Asp Tyr Ala Glu Pro Gly Leu Ile His Ser Ile Gln Leu
    370                 375                 380

gca gtg ttt gcc ctt ggt tat gcc att cgg gat ctg tgt caa gct cgt   1200
Ala Val Phe Ala Leu Gly Tyr Ala Ile Arg Asp Leu Cys Gln Ala Arg
385                 390                 395                 400

gac tgt cag aac ccc aac gcc ttt caa cca tgg gag tta ctt ggt gtg   1248
Asp Cys Gln Asn Pro Asn Ala Phe Gln Pro Trp Glu Leu Leu Gly Val
                405                 410                 415

cta aaa aat gtg aca ttc act gat gga tgg aat tca ttt cat ttt gat   1296
Leu Lys Asn Val Thr Phe Thr Asp Gly Trp Asn Ser Phe His Phe Asp
            420                 425                 430

gct cac ggg gat tta aat act gga tat gat gtt gtg ctc tgg aag gag   1344
Ala His Gly Asp Leu Asn Thr Gly Tyr Asp Val Val Leu Trp Lys Glu
        435                 440                 445

atc aat gga cac atg act gtc act aag atg gca gaa tat gac cta cag   1392
Ile Asn Gly His Met Thr Val Thr Lys Met Ala Glu Tyr Asp Leu Gln
    450                 455                 460

aat gat gtc ttc atc atc cca gat cag gaa aca aaa aat gag ttc agg   1440
Asn Asp Val Phe Ile Ile Pro Asp Gln Glu Thr Lys Asn Glu Phe Arg
465                 470                 475                 480


aat ctt aag caa att caa tct aaa tgc tcc aag gaa tgc agt cct ggg   1488
Asn Leu Lys Gln Ile Gln Ser Lys Cys Ser Lys Glu Cys Ser Pro Gly
                485                 490                 495

caa atg aag aaa act aca aga agt caa cac atc tgt tgc tat gaa tgt   1536
Gln Met Lys Lys Thr Thr Arg Ser Gln His Ile Cys Cys Tyr Glu Cys
            500                 505                 510

cag aac tgt cct gaa aat cat tac act aat cag aca gat atg cct cac   1584
```

```
Gln Asn Cys Pro Glu Asn His Tyr Thr Asn Gln Thr Asp Met Pro His
        515                 520                 525

tgc ctt tta tgc aac aac aaa act cac tgg gcc cct gtt agg agc act   1632
Cys Leu Leu Cys Asn Asn Lys Thr His Trp Ala Pro Val Arg Ser Thr
    530                 535                 540

atg tgc ttt gaa aag gaa gtg gaa tat ctc aac tgg aat gac tcc ttg   1680
Met Cys Phe Glu Lys Glu Val Glu Tyr Leu Asn Trp Asn Asp Ser Leu
545                 550                 555                 560

gcc atc cta ctc ctg att ctc tcc cta ctg gga atc ata ttt gtt ctg   1728
Ala Ile Leu Leu Leu Ile Leu Ser Leu Leu Gly Ile Ile Phe Val Leu
                565                 570                 575

gtt gtt ggc ata ata ttt aca aga aac ctg aac aca cct gtt gtg aaa   1776
Val Val Gly Ile Ile Phe Thr Arg Asn Leu Asn Thr Pro Val Val Lys
            580                 585                 590

tca tcc ggg gga tta aga gtc tgc tat gtg atc ctt ctc tgt cat ttc   1824
Ser Ser Gly Gly Leu Arg Val Cys Tyr Val Ile Leu Leu Cys His Phe
        595                 600                 605

ctc aat ttt gcc agc acg agc ttt ttc att gga gaa cca caa gac ttc   1872
Leu Asn Phe Ala Ser Thr Ser Phe Phe Ile Gly Glu Pro Gln Asp Phe
    610                 615                 620

aca tgt aaa acc agg cag aca atg ttt gga gtg agc ttt act ctt tgc   1920
Thr Cys Lys Thr Arg Gln Thr Met Phe Gly Val Ser Phe Thr Leu Cys
625                 630                 635                 640

atc tcc tgc att ttg acg aag tct ctg aaa att ttg cta gcc ttc agc   1968
Ile Ser Cys Ile Leu Thr Lys Ser Leu Lys Ile Leu Leu Ala Phe Ser
                645                 650                 655

ttt gat ccc aaa tta cag aaa ttt ctg aag tgc ctc tat aga ccg atc   2016
Phe Asp Pro Lys Leu Gln Lys Phe Leu Lys Cys Leu Tyr Arg Pro Ile
            660                 665                 670

ctt att atc ttc act tgc acg ggc atc cag gtt gtc att tgc aca ctc   2064
Leu Ile Ile Phe Thr Cys Thr Gly Ile Gln Val Val Ile Cys Thr Leu
        675                 680                 685

tgg cta atc ttt gca gca cct act gta gag gtg aat gtc tcc ttg ccc   2112
Trp Leu Ile Phe Ala Ala Pro Thr Val Glu Val Asn Val Ser Leu Pro
    690                 695                 700

aga gtc atc atc ctg gag tgt gag gag gga tcc ata ctt gca ttt ggc   2160
Arg Val Ile Ile Leu Glu Cys Glu Glu Gly Ser Ile Leu Ala Phe Gly
705                 710                 715                 720


acc atg ctg ggc tac att gcc atc ctg gcc ttc att tgc ttc ata ttt   2208
Thr Met Leu Gly Tyr Ile Ala Ile Leu Ala Phe Ile Cys Phe Ile Phe
                725                 730                 735

gct ttc aaa ggc aaa tat gag aat tac aat gaa gcc aaa ttc att aca   2256
Ala Phe Lys Gly Lys Tyr Glu Asn Tyr Asn Glu Ala Lys Phe Ile Thr
            740                 745                 750

ttt ggc atg ctc att tac ttc ata gct tgg atc aca ttc atc cct atc   2304
Phe Gly Met Leu Ile Tyr Phe Ile Ala Trp Ile Thr Phe Ile Pro Ile
```

```
        755                 760                 765

tat gct acc aca ttt ggc aaa tat gta cca gct gtg gag att att gtc   2352
Tyr Ala Thr Thr Phe Gly Lys Tyr Val Pro Ala Val Glu Ile Ile Val
    770                 775                 780

ata tta ata tct aac tat gga atc ctg tat tgc aca ttc atc ccc aaa   2400
Ile Leu Ile Ser Asn Tyr Gly Ile Leu Tyr Cys Thr Phe Ile Pro Lys
785                 790                 795                 800

tgc tat gtt att att tgt aag caa gag att aac aca aag tct gcc ttt   2448
Cys Tyr Val Ile Ile Cys Lys Gln Glu Ile Asn Thr Lys Ser Ala Phe
                805                 810                 815

ctc aag                                                          2454
Leu Lys
```

<210> 68
<211> 818
<212> PRT
<213> Homo sapiens

<400> 68

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Gly His Ile Ile Ile Gly Gly Leu Phe Ala Ile His Glu Lys Met Leu
 1               5                  10                  15
Ser Ser Glu Asp Ser Pro Arg Arg Pro Gln Ile Gln Glu Cys Val Gly
            20                  25                  30
Phe Glu Ile Ser Val Phe Leu Gln Thr Leu Ala Met Ile His Ser Ile
        35                  40                  45
Glu Met Ile Asn Asn Ser Thr Leu Leu Pro Gly Val Lys Leu Gly Tyr
    50                  55                  60
Glu Ile Tyr Asp Thr Cys Thr Glu Val Thr Val Ala Met Ala Ala Thr
65                  70                  75                  80
Leu Arg Phe Leu Ser Lys Phe Asn Cys Ser Arg Glu Thr Val Glu Phe
                85                  90                  95
Lys Cys Asp Tyr Ser Ser Tyr Met Pro Arg Val Lys Ala Val Ile Gly
            100                 105                 110
Ser Gly Tyr Ser Glu Ile Thr Met Ala Val Ser Arg Met Leu Asn Leu
        115                 120                 125
Gln Leu Met Pro Gln Val Gly Tyr Glu Ser Thr Ala Glu Ile Leu Ser
    130                 135                 140
Asp Lys Ile Arg Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Phe
145                 150                 155                 160
His Gln Ile Lys Ala Met Ala His Leu Ile Gln Lys Ser Gly Trp Asn
                165                 170                 175
Trp Ile Gly Ile Ile Thr Thr Asp Asp Asp Tyr Gly Arg Leu Ala Leu
            180                 185                 190
Asn Thr Phe Ile Ile Gln Ala Glu Ala Asn Asn Val Cys Ile Ala Phe
        195                 200                 205

Lys Glu Val Leu Pro Ala Phe Leu Ser Asp Asn Thr Ile Glu Val Arg
    210                 215                 220
Ile Asn Arg Thr Leu Lys Lys Ile Ile Leu Glu Ala Gln Val Asn Val
225                 230                 235                 240
Ile Val Val Phe Leu Arg Gln Phe His Val Phe Asp Leu Phe Asn Lys
                245                 250                 255
Ala Ile Glu Met Asn Ile Asn Lys Met Trp Ile Ala Ser Asp Asn Trp
            260                 265                 270
Ser Thr Ala Thr Lys Ile Thr Thr Ile Pro Asn Val Lys Lys Ile Gly
        275                 280                 285
Lys Val Val Gly Phe Ala Phe Arg Arg Gly Asn Ile Ser Ser Phe His
```

```
    290                 295                 300
Ser Phe Leu Gln Asn Leu His Leu Leu Pro Ser Asp Ser His Lys Leu
305                 310                 315                 320
Leu His Glu Tyr Ala Met His Leu Ser Ala Cys Ala Tyr Val Lys Asp
                325                 330                 335
Thr Asp Leu Ser Gln Cys Ile Phe Asn His Ser Gln Arg Thr Leu Ala
            340                 345                 350
Tyr Lys Ala Asn Lys Ala Ile Glu Arg Asn Phe Val Met Arg Asn Asp
        355                 360                 365
Phe Leu Trp Asp Tyr Ala Glu Pro Gly Leu Ile His Ser Ile Gln Leu
    370                 375                 380
Ala Val Phe Ala Leu Gly Tyr Ala Ile Arg Asp Leu Cys Gln Ala Arg
385                 390                 395                 400
Asp Cys Gln Asn Pro Asn Ala Phe Gln Pro Trp Glu Leu Leu Gly Val
                405                 410                 415
Leu Lys Asn Val Thr Phe Thr Asp Gly Trp Asn Ser Phe His Phe Asp
            420                 425                 430
Ala His Gly Asp Leu Asn Thr Gly Tyr Asp Val Val Leu Trp Lys Glu
        435                 440                 445
Ile Asn Gly His Met Thr Val Thr Lys Met Ala Glu Tyr Asp Leu Gln
    450                 455                 460
Asn Asp Val Phe Ile Ile Pro Asp Gln Glu Thr Lys Asn Glu Phe Arg
465                 470                 475                 480
Asn Leu Lys Gln Ile Gln Ser Lys Cys Ser Lys Glu Cys Ser Pro Gly
                485                 490                 495
Gln Met Lys Lys Thr Thr Arg Ser Gln His Ile Cys Cys Tyr Glu Cys
            500                 505                 510
Gln Asn Cys Pro Glu Asn His Tyr Thr Asn Gln Thr Asp Met Pro His
        515                 520                 525
Cys Leu Leu Cys Asn Asn Lys Thr His Trp Ala Pro Val Arg Ser Thr
    530                 535                 540
Met Cys Phe Glu Lys Glu Val Glu Tyr Leu Asn Trp Asn Asp Ser Leu
545                 550                 555                 560
Ala Ile Leu Leu Leu Ile Leu Ser Leu Leu Gly Ile Ile Phe Val Leu
                565                 570                 575
Val Val Gly Ile Ile Phe Thr Arg Asn Leu Asn Thr Pro Val Val Lys
            580                 585                 590
Ser Ser Gly Gly Leu Arg Val Cys Tyr Val Ile Leu Leu Cys His Phe
        595                 600                 605
Leu Asn Phe Ala Ser Thr Ser Phe Phe Ile Gly Glu Pro Gln Asp Phe
    610                 615                 620
Thr Cys Lys Thr Arg Gln Thr Met Phe Gly Val Ser Phe Thr Leu Cys
625                 630                 635                 640
Ile Ser Cys Ile Leu Thr Lys Ser Leu Lys Ile Leu Leu Ala Phe Ser
                645                 650                 655
Phe Asp Pro Lys Leu Gln Lys Phe Leu Lys Cys Leu Tyr Arg Pro Ile
            660                 665                 670
Leu Ile Ile Phe Thr Cys Thr Gly Ile Gln Val Val Ile Cys Thr Leu
        675                 680                 685
Trp Leu Ile Phe Ala Ala Pro Thr Val Glu Val Asn Val Ser Leu Pro
    690                 695                 700
Arg Val Ile Ile Leu Glu Cys Glu Glu Gly Ser Ile Leu Ala Phe Gly
705                 710                 715                 720
Thr Met Leu Gly Tyr Ile Ala Ile Leu Ala Phe Ile Cys Phe Ile Phe
                725                 730                 735
Ala Phe Lys Gly Lys Tyr Glu Asn Tyr Asn Glu Ala Lys Phe Ile Thr
            740                 745                 750
Phe Gly Met Leu Ile Tyr Phe Ile Ala Trp Ile Thr Phe Ile Pro Ile
        755                 760                 765
Tyr Ala Thr Thr Phe Gly Lys Tyr Val Pro Ala Val Glu Ile Ile Val
    770                 775                 780
Ile Leu Ile Ser Asn Tyr Gly Ile Leu Tyr Cys Thr Phe Ile Pro Lys
785                 790                 795                 800
```

```
Cys Tyr Val Ile Ile Cys Lys Gln Glu Ile Asn Thr Lys Ser Ala Phe
                805                 810                 815
Leu Lys
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<210> 69
<211> 2376
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2376)

<400> 69

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ggc aga cta gtc gta gga gcc ctt ttt aat cta gaa agt tgg tac caa   48
Gly Arg Leu Val Val Gly Ala Leu Phe Asn Leu Glu Ser Trp Tyr Gln
 1               5                  10                  15

gaa gca tgt cct gag att tat tgt ttt cat cct ccc acc tgc cta ggc   96
Glu Ala Cys Pro Glu Ile Tyr Cys Phe His Pro Pro Thr Cys Leu Gly
            20                  25                  30

ttc aat gag cat ggc tac cac ctc ttc cag gct atg cgg ctt ggg gtt   144
Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg Leu Gly Val
        35                  40                  45

gag gag ata aac aac tcc acg gcc ctg ctg ccc aac atc acc ctg ggg   192
Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile Thr Leu Gly
    50                  55                  60

tac cag ctg tat gat gtg tgt tct gac tct gcc aat gtg tat gcc acg   240
Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val Tyr Ala Thr
65                  70                  75                  80

ctg aga gtg ctc tcc ctg cca ggg caa cac cac ata gag ctc caa gga   288
Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu Leu Gln Gly
                85                  90                  95

gac ctt ctc cac tat tcc cct acg gtg ctg gca gtg att ggg cct gac   336
Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile Gly Pro Asp
            100                 105                 110

agc acc aac cgt gct gcc acc aca gcc gcc ctg ctg agc cct ttc ctg   384
Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser Pro Phe Leu
        115                 120                 125

gtg ccc atg att agc tat gcg gcc agc agc gag acg ctc agc gtg aag   432
Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu Ser Val Lys
    130                 135                 140

cgg cag tat ccc tct ttc ctg cgc acc atc ccc aat gac aag tac cag   480
Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp Lys Tyr Gln
145                 150                 155                 160

gtg gag acc atg gtg ctg ctg ctg cag aag ttc ggg tgg acc tgg atc   528
Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp Thr Trp Ile
                165                 170                 175

tct ctg gtt ggc agc agt gac gac tat ggg cag cta ggg gtg cag gca   576
```

```
Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly Val Gln Ala
            180                 185                 190

ctg gag aac cag gcc act ggt cag ggg atc tgc att gct ttc aag gac   624
Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala Phe Lys Asp
        195                 200                 205

atc atg ccc ttc tct gcc cag gtg ggc gat gag agg atg cag tgc ctc   672
Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met Gln Cys Leu
    210                 215                 220

atg cgc cac ctg gcc cag gcc ggg gcc acc gtc gtg gtt gtt ttt tcc   720
Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val Val Phe Ser
225                 230                 235                 240

agc cgg cag ttg gcc agg gtg ttt ttc gag tcc gtg gtg ctg acc aac   768
Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val Leu Thr Asn
                245                 250                 255

ctg act ggc aag gtg tgg gtc gcc tca gaa gcc tgg gcc ctc tcc agg   816
Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala Leu Ser Arg
            260                 265                 270

cac atc act ggg gtg ccc ggg atc cag cgc att ggg atg gtg ctg ggc   864
His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met Val Leu Gly
        275                 280                 285

gtg gcc atc cag aag agg gct gtc cct ggc ctg aag gcg ttt gaa gaa   912
Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala Phe Glu Glu
    290                 295                 300

gcc tat gcc cgg gca gac aag aag gcc cct agg cct tgc cac aag ggc   960
Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys His Lys Gly
305                 310                 315                 320

tcc tgg tgc agc agc aat cag ctc tgc aga gaa tgc caa gct ttc atg   1008
Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln Ala Phe Met
                325                 330                 335

gca cac acg atg ccc aag ctc aaa gcc ttc tcc atg agt tct gcc tac   1056
Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser Ser Ala Tyr
            340                 345                 350

aac gca tac cgg gct gtg tat gcg gtg gcc cat ggc ctc cac cag ctc   1104
Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu His Gln Leu
        355                 360                 365


ctg ggc tgt gcc tct gga gct tgt tcc agg ggc cga gtc tac ccc tgg   1152
Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val Tyr Pro Trp
    370                 375                 380

cag ctt ttg gag cag atc cac aag gtg cat ttc ctt cta cac aag gac   1200
Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu His Lys Asp
385                 390                 395                 400

act gtg gcg ttt aat gac aac aga gat ccc ctc agt agc tat aac ata   1248
Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser Tyr Asn Ile
                405                 410                 415

att gcc tgg gac tgg aat gga ccc aag tgg acc ttc acg gtc ctc ggt   1296
Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr Val Leu Gly
```

```
            420                 425                 430

tcc tcc aca tgg tct cca gtt cag cta aac ata aat gag acc aaa atc   1344
Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu Thr Lys Ile
        435                 440                 445

cag tgg cac gga aag gac aac cag gtg cct aag tct gtg tgt tcc agc   1392
Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val Cys Ser Ser
    450                 455                 460

gac tgt ctt gaa ggg cac cag cga gtg gtt acg ggt ttc cat cac tgc   1440
Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe His His Cys
465                 470                 475                 480

tgc ttt gag tgt gtg ccc tgt ggg gct ggg acc ttc ctc aac aag agt   1488
Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu Asn Lys Ser
                485                 490                 495

ggt gaa tgc cag cct tgt ggg aaa gaa gag tgg gca cct gag gga agc   1536
Gly Glu Cys Gln Pro Cys Gly Lys Glu Glu Trp Ala Pro Glu Gly Ser
            500                 505                 510

cag acc tgc ttc ccg cgc act gtg gtg ttt ttg gct ttg cgt gag cac   1584
Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu Ala Leu Arg Glu His
        515                 520                 525

acc tct tgg gtg ctg ctg gca gct aac acg ctg ctg ctg ctg ctg ctg   1632
Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu Leu Leu Leu Leu Leu
    530                 535                 540

ctt ggg act gct ggc ctg ttt gcc tgg cac cta gac acc cct gtg gtg   1680
Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu Asp Thr Pro Val Val
545                 550                 555                 560

agg tca gca ggg ggc cgc ctg tgc ttt ctt atg ctg ggc tcc ctg gca   1728
Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu Gly Ser Leu Ala
                565                 570                 575

gca ggt agt ggc agc ctc tat ggc ttc ttt ggg gaa ccc aca agg cct   1776
Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly Glu Pro Thr Arg Pro
            580                 585                 590

gcg tgc ttg cta cgc cag gcc ctc ttt gcc ctt ggt ttc acc atc ttc   1824
Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu Gly Phe Thr Ile Phe
        595                 600                 605


ctg tcc tgc ctg aca gtt cgc tca ttc caa cta atc atc atc ttc aag   1872
Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu Ile Ile Ile Phe Lys
    610                 615                 620

ttt tcc acc aag gta cct aca ttc tac cac gcc tgg gtc caa aac cac   1920
Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala Trp Val Gln Asn His
625                 630                 635                 640

ggt gct ggc ctg ttt gtg atg atc agc tca gcg gcc cag ctg ctt atc   1968
Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala Ala Gln Leu Leu Ile
                645                 650                 655

tgt cta act tgg ctg gtg gtg tgg acc cca ctg cct gct agg gaa tac   2016
Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu Pro Ala Arg Glu Tyr
            660                 665                 670
```

```
cag cgc ttc ccc cat ctg gtg atg ctt gag tgc aca gag acc aac tcc   2064
Gln Arg Phe Pro His Leu Val Met Leu Glu Cys Thr Glu Thr Asn Ser
        675                 680                 685

ctg ggc ttc ata ctg gcc ttc ctc tac aat ggc ctc ctc tcc atc agt   2112
Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly Leu Leu Ser Ile Ser
    690                 695                 700

gcc ttt gcc tgc agc tac ctg ggt aag gac ttg cca gag aac tac aac   2160
Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu Pro Glu Asn Tyr Asn
705                 710                 715                 720

gag gcc aaa tgt gtc acc ttc agc ctg ctc ttc aac ttc gtg tcc tgg   2208
Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe Asn Phe Val Ser Trp
                725                 730                 735

atc gcc ttc ttc acc acg gcc agc gtc tac gac ggc aag tac ctg cct   2256
Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp Gly Lys Tyr Leu Pro
            740                 745                 750

gcg gcc aac atg atg gct ggg ctg agc agc ctg agc agc ggc ttc ggt   2304
Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu Ser Ser Gly Phe Gly
        755                 760                 765

ggg tat ttt ctg cct aag tgc tac gtg atc ctc tgc cgc cca gac ctc   2352
Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys Arg Pro Asp Leu
    770                 775                 780

aac agc aca gag cac ttc cag gcc                                   2376
Asn Ser Thr Glu His Phe Gln Ala
785                 790
```

<210> 70
<211> 792
<212> PRT
<213> Homo sapiens

<400> 70

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Gly Arg Leu Val Val Gly Ala Leu Phe Asn Leu Glu Ser Trp Tyr Gln
 1               5                  10                  15
Glu Ala Cys Pro Glu Ile Tyr Cys Phe His Pro Pro Thr Cys Leu Gly
            20                  25                  30
Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg Leu Gly Val
        35                  40                  45

Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile Thr Leu Gly
    50                  55                  60
Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val Tyr Ala Thr
65                  70                  75                  80
Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu Leu Gln Gly
                85                  90                  95
Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile Gly Pro Asp
            100                 105                 110
Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser Pro Phe Leu
        115                 120                 125
Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu Ser Val Lys
    130                 135                 140
Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp Lys Tyr Gln
145                 150                 155                 160
Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp Thr Trp Ile
                165                 170                 175
```

```
Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly Val Gln Ala
            180                 185                 190
Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala Phe Lys Asp
        195                 200                 205
Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met Gln Cys Leu
    210                 215                 220
Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val Val Phe Ser
225                 230                 235                 240
Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val Leu Thr Asn
                245                 250                 255
Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala Leu Ser Arg
            260                 265                 270
His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met Val Leu Gly
        275                 280                 285
Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala Phe Glu Glu
    290                 295                 300
Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys His Lys Gly
305                 310                 315                 320
Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln Ala Phe Met
                325                 330                 335
Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser Ser Ala Tyr
            340                 345                 350
Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu His Gln Leu
        355                 360                 365
Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val Tyr Pro Trp
    370                 375                 380
Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu His Lys Asp
385                 390                 395                 400
Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser Tyr Asn Ile
                405                 410                 415
Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr Val Leu Gly
            420                 425                 430
Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu Thr Lys Ile
        435                 440                 445
Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val Cys Ser Ser
    450                 455                 460
Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe His His Cys
465                 470                 475                 480
Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu Asn Lys Ser
                485                 490                 495
Gly Glu Cys Gln Pro Cys Gly Lys Glu Glu Trp Ala Pro Glu Gly Ser
            500                 505                 510
Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu Ala Leu Arg Glu His
        515                 520                 525
Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu Leu Leu Leu Leu Leu
    530                 535                 540
Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu Asp Thr Pro Val Val
545                 550                 555                 560
Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu Gly Ser Leu Ala
                565                 570                 575
Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly Glu Pro Thr Arg Pro
            580                 585                 590
Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu Gly Phe Thr Ile Phe
        595                 600                 605
Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu Ile Ile Ile Phe Lys
    610                 615                 620
Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala Trp Val Gln Asn His
625                 630                 635                 640
Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala Ala Gln Leu Leu Ile
                645                 650                 655
Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu Pro Ala Arg Glu Tyr
            660                 665                 670
Gln Arg Phe Pro His Leu Val Met Leu Glu Cys Thr Glu Thr Asn Ser
```

```
        675                 680                 685
Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly Leu Leu Ser Ile Ser
    690                 695                 700
Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu Pro Glu Asn Tyr Asn
705                 710                 715                 720
Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe Asn Phe Val Ser Trp
                725                 730                 735
Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp Gly Lys Tyr Leu Pro
            740                 745                 750
Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu Ser Ser Gly Phe Gly
        755                 760                 765
Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys Arg Pro Asp Leu
    770                 775                 780
Asn Ser Thr Glu His Phe Gln Ala
785                 790


<210> 71
<211> 2415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2415)

<400> 71
ggg gac tac gtg ctg ggg ggg ctg ttc ccc ctg ggc gag gcc gag gag   48
Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
 1               5                  10                  15

gct ggc ctc cgc agc cgg aca cgg ccc agc agc cct gtg tgc acc agg   96
Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
            20                  25                  30

ttc tcc tca aac ggc ctg ctc tgg gca ctg gcc atg aaa atg gcc gtg   144
Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
        35                  40                  45

gag gag atc aac aac aag tcg gat ctg ctg ccc ggg ctg cgc ctg ggc   192
Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
    50                  55                  60



tac gac ctc ttt gat acg tgc tcg gag cct gtg gtg gcc atg aag ccc   240
Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
65                  70                  75                  80

agc ctc atg ttc ctg gcc aag gca ggc agc cgc gac atc gcc gcc tac   288
Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
                85                  90                  95

tgc aac tac acg cag tac cag ccc cgt gtg ctg gct gtc atc ggg ccc   336
Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
            100                 105                 110

cac tcg tca gag ctc gcc atg gtc acc ggg aag ttc ttc agc ttc ttc   384
His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
        115                 120                 125

ctc atg ccc caa tgc ctc ttg gcc ttg cag gtc agc tac ggt gct agc   432
Leu Met Pro Gln Cys Leu Leu Ala Leu Gln Val Ser Tyr Gly Ala Ser
```

```
    130                 135                 140

atg gag ctg ctg agc gcc cgg gag acc ttc ccc tcc ttc ttc cgc acc   480
Met Glu Leu Leu Ser Ala Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr
145                 150                 155                 160

gtg ccc agc gac cgt gtg cag ctg acg gcc gcc gcg gag ctg ctg cag   528
Val Pro Ser Asp Arg Val Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln
                165                 170                 175

gag ttc ggc tgg aac tgg gtg gcc gcc ctg ggc agc gac gac gag tac   576
Glu Phe Gly Trp Asn Trp Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr
            180                 185                 190

ggc cgg cag ggc ctg agc atc ttc tcg gcc ctg gcc gcg gca cgc ggc   624
Gly Arg Gln Gly Leu Ser Ile Phe Ser Ala Leu Ala Ala Ala Arg Gly
        195                 200                 205

atc tgc atc gcg cac gag ggc ctg gtg ccg ctg ccc cgt gcc gat gac   672
Ile Cys Ile Ala His Glu Gly Leu Val Pro Leu Pro Arg Ala Asp Asp
    210                 215                 220

tcg cgg ctg ggg aag gtg cag gac gtc ctg cac cag gtg aac cag agc   720
Ser Arg Leu Gly Lys Val Gln Asp Val Leu His Gln Val Asn Gln Ser
225                 230                 235                 240

agc gtg cag gtg gtg ctg ctg ttc gcc tcc gtg cac gcc gcc cac gcc   768
Ser Val Gln Val Val Leu Leu Phe Ala Ser Val His Ala Ala His Ala
                245                 250                 255

ctc ttc aac tac agc atc agc agc agg ctc tcg ccc aag gtg tgg gtg   816
Leu Phe Asn Tyr Ser Ile Ser Ser Arg Leu Ser Pro Lys Val Trp Val
            260                 265                 270

gcc agc gag gcc tgg ctg acc tct gac ctg gtc atg ggg ctg ccc ggc   864
Ala Ser Glu Ala Trp Leu Thr Ser Asp Leu Val Met Gly Leu Pro Gly
        275                 280                 285

atg gcc cag atg ggc acg gtg ctt ggc ttc ctc cag agg ggt gcc cag   912
Met Ala Gln Met Gly Thr Val Leu Gly Phe Leu Gln Arg Gly Ala Gln
    290                 295                 300


ctg cac gag ttc ccc cag tac gtg aag acg cac ctg gcc ctg gcc acc   960
Leu His Glu Phe Pro Gln Tyr Val Lys Thr His Leu Ala Leu Ala Thr
305                 310                 315                 320

gac ccg gcc ttc tgc tct gcc ctg ggc gag agg gag cag ggt ctg gag  1008
Asp Pro Ala Phe Cys Ser Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu
                325                 330                 335

gag gac gtg gtg ggc cag cgc tgc ccg cag tgt gac tgc atc acg ctg  1056
Glu Asp Val Val Gly Gln Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu
            340                 345                 350

cag aac gtg agc gca ggg cta aat cac cac cag acg ttc tct gtc tac  1104
Gln Asn Val Ser Ala Gly Leu Asn His His Gln Thr Phe Ser Val Tyr
        355                 360                 365

gca gct gtg tat agc gtg gcc cag gcc ctg cac aac act ctt cag tgc  1152
Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln Cys
    370                 375                 380
```

```
aac gcc tca ggc tgc ccc gcg cag gac ccc gtg aag ccc tgg cag ctc   1200
Asn Ala Ser Gly Cys Pro Ala Gln Asp Pro Val Lys Pro Trp Gln Leu
385                 390                 395                 400

ctg gag aac atg tac aac ctg acc ttc cac gtg ggc ggg ctg ccg ctg   1248
Leu Glu Asn Met Tyr Asn Leu Thr Phe His Val Gly Gly Leu Pro Leu
                405                 410                 415

cgg ttc gac agc agc gga aac gtg gac atg gag tac gac ctg aag ctg   1296
Arg Phe Asp Ser Ser Gly Asn Val Asp Met Glu Tyr Asp Leu Lys Leu
            420                 425                 430

tgg gtg tgg cag ggc tca gtg ccc agg ctc cac gac gtg ggc agg ttc   1344
Trp Val Trp Gln Gly Ser Val Pro Arg Leu His Asp Val Gly Arg Phe
        435                 440                 445

aac ggc agc ctc agg aca gag cgc ctg aag atc cgc tgg cac acg tct   1392
Asn Gly Ser Leu Arg Thr Glu Arg Leu Lys Ile Arg Trp His Thr Ser
    450                 455                 460

gac aac cag aag ccc gtg tcc cgg tgc tcg cgg cag tgc cag gag ggc   1440
Asp Asn Gln Lys Pro Val Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly
465                 470                 475                 480

cag gtg cgc cgg gtc aag ggg ttc cac tcc tgc tgc tac gac tgt gtg   1488
Gln Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val
                485                 490                 495

gac tgc gag gcg ggc agc tac cgg caa aac cca gac gac atc gcc tgc   1536
Asp Cys Glu Ala Gly Ser Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys
            500                 505                 510

acc ttt tgt ggc cag gat gag tgg tcc ccg gag cga agc aca cgc tgc   1584
Thr Phe Cys Gly Gln Asp Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys
        515                 520                 525

ttc cgc cgc agg tct cgg ttc ctg gca tgg ggc gag ccg gct gtg ctg   1632
Phe Arg Arg Arg Ser Arg Phe Leu Ala Trp Gly Glu Pro Ala Val Leu
    530                 535                 540


ctg ctg ctc ctg ctg ctg agc ctg gcg ctg ggc ctt gtg ctg gct gct   1680
Leu Leu Leu Leu Leu Leu Ser Leu Ala Leu Gly Leu Val Leu Ala Ala
545                 550                 555                 560

ttg ggg ctg ttc gtt cac cat cgg gac agc cca ctg gtt cag gcc tcg   1728
Leu Gly Leu Phe Val His His Arg Asp Ser Pro Leu Val Gln Ala Ser
                565                 570                 575

ggg ggg ccc ctg gcc tgc ttt ggc ctg gtg tgc ctg ggc ctg gtc tgc   1776
Gly Gly Pro Leu Ala Cys Phe Gly Leu Val Cys Leu Gly Leu Val Cys
            580                 585                 590

ctc agc gtc ctc ctg ttc cct ggc cag ccc agc cct gcc cga tgc ctg   1824
Leu Ser Val Leu Leu Phe Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu
        595                 600                 605

gcc cag cag ccc ttg tcc cac ctc ccg ctc acg ggc tgc ctg agc aca   1872
Ala Gln Gln Pro Leu Ser His Leu Pro Leu Thr Gly Cys Leu Ser Thr
    610                 615                 620
```

```
ctc ttc ctg cag gcg gcc gag atc ttc gtg gag tca gaa ctg cct ctg   1920
Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu
625                 630                 635                 640

agc tgg gca gac cgg ctg agt ggc tgc ctg cgg ggg ccc tgg gcc tgg   1968
Ser Trp Ala Asp Arg Leu Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp
                645                 650                 655

ctg gtg gtg ctg ctg gcc atg ctg gtg gag gtc gca ctg tgc acc tgg   2016
Leu Val Val Leu Leu Ala Met Leu Val Glu Val Ala Leu Cys Thr Trp
            660                 665                 670

tac ctg gtg gcc ttc ccg ccg gag gtg gtg acg gac tgg cac atg ctg   2064
Tyr Leu Val Ala Phe Pro Pro Glu Val Val Thr Asp Trp His Met Leu
        675                 680                 685

ccc acg gag gcg ctg gtg cac tgc cgc aca cgc tcc tgg gtc agc ttc   2112
Pro Thr Glu Ala Leu Val His Cys Arg Thr Arg Ser Trp Val Ser Phe
    690                 695                 700

ggc cta gcg cac gcc acc aat gcc acg ctg gcc ttt ctc tgc ttc ctg   2160
Gly Leu Ala His Ala Thr Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu
705                 710                 715                 720

ggc act ttc ctg gtg cgg agc cag ccg ggc tgc tac aac cgt gcc cgt   2208
Gly Thr Phe Leu Val Arg Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg
                725                 730                 735

ggc ctc acc ttt gcc atg ctg gcc tac ttc atc acc tgg gtc tcc ttt   2256
Gly Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe
            740                 745                 750

gtg ccc ctc ctg gcc aat gtg cag gtg gtc ctc agg ccc gcc gtg cag   2304
Val Pro Leu Leu Ala Asn Val Gln Val Val Leu Arg Pro Ala Val Gln
        755                 760                 765

atg ggc gcc ctc ctg ctc tgt gtc ctg ggc atc ctg gct gcc ttc cac   2352
Met Gly Ala Leu Leu Leu Cys Val Leu Gly Ile Leu Ala Ala Phe His
    770                 775                 780



ctg ccc agg tgt tac ctg ctc atg cgg cag cca ggg ctc aac acc ccc   2400
Leu Pro Arg Cys Tyr Leu Leu Met Arg Gln Pro Gly Leu Asn Thr Pro
785                 790                 795                 800

gag ttc ttc ctg gga                                               2415
Glu Phe Phe Leu Gly
                805
```

<210> 72
<211> 805
<212> PRT
<213> Homo sapiens

<400> 72

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Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
 1               5                  10                  15
Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
            20                  25                  30
Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
        35                  40                  45
```

```
Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
    50                  55                  60
Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
65                  70                  75                  80
Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
                85                  90                  95
Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
            100                 105                 110
His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
        115                 120                 125
Leu Met Pro Gln Cys Leu Leu Ala Leu Gln Val Ser Tyr Gly Ala Ser
    130                 135                 140
Met Glu Leu Leu Ser Ala Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr
145                 150                 155                 160
Val Pro Ser Asp Arg Val Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln
                165                 170                 175
Glu Phe Gly Trp Asn Trp Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr
            180                 185                 190
Gly Arg Gln Gly Leu Ser Ile Phe Ser Ala Leu Ala Ala Ala Arg Gly
        195                 200                 205
Ile Cys Ile Ala His Glu Gly Leu Val Pro Leu Pro Arg Ala Asp Asp
    210                 215                 220
Ser Arg Leu Gly Lys Val Gln Asp Val Leu His Gln Val Asn Gln Ser
225                 230                 235                 240
Ser Val Gln Val Val Leu Leu Phe Ala Ser Val His Ala Ala His Ala
                245                 250                 255
Leu Phe Asn Tyr Ser Ile Ser Ser Arg Leu Ser Pro Lys Val Trp Val
            260                 265                 270
Ala Ser Glu Ala Trp Leu Thr Ser Asp Leu Val Met Gly Leu Pro Gly
        275                 280                 285
Met Ala Gln Met Gly Thr Val Leu Gly Phe Leu Gln Arg Gly Ala Gln
    290                 295                 300
Leu His Glu Phe Pro Gln Tyr Val Lys Thr His Leu Ala Leu Ala Thr
305                 310                 315                 320
Asp Pro Ala Phe Cys Ser Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu
                325                 330                 335
Glu Asp Val Val Gly Gln Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu
            340                 345                 350
Gln Asn Val Ser Ala Gly Leu Asn His His Gln Thr Phe Ser Val Tyr
        355                 360                 365

Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln Cys
    370                 375                 380
Asn Ala Ser Gly Cys Pro Ala Gln Asp Pro Val Lys Pro Trp Gln Leu
385                 390                 395                 400
Leu Glu Asn Met Tyr Asn Leu Thr Phe His Val Gly Gly Leu Pro Leu
                405                 410                 415
Arg Phe Asp Ser Ser Gly Asn Val Asp Met Glu Tyr Asp Leu Lys Leu
            420                 425                 430
Trp Val Trp Gln Gly Ser Val Pro Arg Leu His Asp Val Gly Arg Phe
        435                 440                 445
Asn Gly Ser Leu Arg Thr Glu Arg Leu Lys Ile Arg Trp His Thr Ser
    450                 455                 460
Asp Asn Gln Lys Pro Val Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly
465                 470                 475                 480
Gln Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val
                485                 490                 495
Asp Cys Glu Ala Gly Ser Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys
            500                 505                 510
Thr Phe Cys Gly Gln Asp Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys
        515                 520                 525
Phe Arg Arg Arg Ser Arg Phe Leu Ala Trp Gly Glu Pro Ala Val Leu
    530                 535                 540
```

```
Leu Leu Leu Leu Leu Leu Ser Leu Ala Leu Gly Leu Val Leu Ala Ala
545                 550                 555                 560
Leu Gly Leu Phe Val His His Arg Asp Ser Pro Leu Val Gln Ala Ser
                565                 570                 575
Gly Gly Pro Leu Ala Cys Phe Gly Leu Val Cys Leu Gly Leu Val Cys
            580                 585                 590
Leu Ser Val Leu Leu Phe Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu
        595                 600                 605
Ala Gln Gln Pro Leu Ser His Leu Pro Leu Thr Gly Cys Leu Ser Thr
    610                 615                 620
Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu
625                 630                 635                 640
Ser Trp Ala Asp Arg Leu Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp
                645                 650                 655
Leu Val Val Leu Leu Ala Met Leu Val Glu Val Ala Leu Cys Thr Trp
            660                 665                 670
Tyr Leu Val Ala Phe Pro Pro Glu Val Val Thr Asp Trp His Met Leu
        675                 680                 685
Pro Thr Glu Ala Leu Val His Cys Arg Thr Arg Ser Trp Val Ser Phe
    690                 695                 700
Gly Leu Ala His Ala Thr Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu
705                 710                 715                 720
Gly Thr Phe Leu Val Arg Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg
                725                 730                 735
Gly Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe
            740                 745                 750
Val Pro Leu Leu Ala Asn Val Gln Val Val Leu Arg Pro Ala Val Gln
        755                 760                 765
Met Gly Ala Leu Leu Leu Cys Val Leu Gly Ile Leu Ala Ala Phe His
    770                 775                 780
Leu Pro Arg Cys Tyr Leu Leu Met Arg Gln Pro Gly Leu Asn Thr Pro
785                 790                 795                 800
Glu Phe Phe Leu Gly
                805
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<210> 73
<211> 1857
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1857)

<400> 73

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gcc ttg gcg ctg ctg cag cgc tct agc ggc gct gcg gcc gcc tcg gcc   48
Ala Leu Ala Leu Leu Gln Arg Ser Ser Gly Ala Ala Ala Ala Ser Ala
 1               5                  10                  15

aag gag ctg gca tgc caa gag atc acc gtg ccg ctg tgt aag ggc atc   96
Lys Glu Leu Ala Cys Gln Glu Ile Thr Val Pro Leu Cys Lys Gly Ile
            20                  25                  30

ggc tac aac tac acc tac atg ccc aat cag ttc aac cac gac acg caa   144
Gly Tyr Asn Tyr Thr Tyr Met Pro Asn Gln Phe Asn His Asp Thr Gln
        35                  40                  45

gac gag gcg ggc ctg gag gtg cac cag ttc tgg ccg ctg gtg gag atc   192
Asp Glu Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile
    50                  55                  60

cag tgc tcg ccc gat ctc aag ttc ttc ctg tgc agc atg tac acg ccc   240
```

```
Gln Cys Ser Pro Asp Leu Lys Phe Phe Leu Cys Ser Met Tyr Thr Pro
 65                  70                  75                  80

atc tgc cta gag gac tac aag aag ccg ctg ccg ccc tgc cgc tcg gtg   288
Ile Cys Leu Glu Asp Tyr Lys Lys Pro Leu Pro Pro Cys Arg Ser Val
                 85                  90                  95

tgc gag cgc gcc aag gcc ggc tgc gcg ccg ctc atg cgc cag tac ggc   336
Cys Glu Arg Ala Lys Ala Gly Cys Ala Pro Leu Met Arg Gln Tyr Gly
            100                 105                 110

ttc gcc tgg ccc gac cgc atg cgc tgc gac cgg ctg ccc gag caa ggc   384
Phe Ala Trp Pro Asp Arg Met Arg Cys Asp Arg Leu Pro Glu Gln Gly
        115                 120                 125

aac cct gac acg ctg tgc atg gac tac aac cgc acc gac cta acc acc   432
Asn Pro Asp Thr Leu Cys Met Asp Tyr Asn Arg Thr Asp Leu Thr Thr
    130                 135                 140

gcc gcg ccc agc ccg ccg cgc cgc ctg ccg ccg ccg ccg ccc ggc gag   480
Ala Ala Pro Ser Pro Pro Arg Arg Leu Pro Pro Pro Pro Pro Gly Glu
145                 150                 155                 160

cag ccg cct tcg ggc agc ggc cac ggc cgc ccg ccg ggg gcc agg ccc   528
Gln Pro Pro Ser Gly Ser Gly His Gly Arg Pro Pro Gly Ala Arg Pro
                165                 170                 175

ccg cac cgc ggc ggc ggc agg ggc ggt ggc ggc ggg gac gcg gcg gcg   576
Pro His Arg Gly Gly Gly Arg Gly Gly Gly Gly Gly Asp Ala Ala Ala
            180                 185                 190

ccc cca gct cgc ggc ggc ggc ggt ggc ggg aag gcg cgg ccc cct ggc   624
Pro Pro Ala Arg Gly Gly Gly Gly Gly Gly Lys Ala Arg Pro Pro Gly
        195                 200                 205

ggc ggc gcg gct ccc tgc gag ccc ggg tgc cag tgc cgc gcg cct atg   672
Gly Gly Ala Ala Pro Cys Glu Pro Gly Cys Gln Cys Arg Ala Pro Met
    210                 215                 220


gtg agc gtg tcc agc gag cgc cac ccg ctc tac aac cgc gtc aag aca   720
Val Ser Val Ser Ser Glu Arg His Pro Leu Tyr Asn Arg Val Lys Thr
225                 230                 235                 240

ggc cag atc gct aac tgc gcg ctg ccc tgc cac aac ccc ttt ttc agc   768
Gly Gln Ile Ala Asn Cys Ala Leu Pro Cys His Asn Pro Phe Phe Ser
                245                 250                 255

cag gac gag cgc gcc ttc acc gtc ttc tgg atc ggc ctg tgg tcg gtg   816
Gln Asp Glu Arg Ala Phe Thr Val Phe Trp Ile Gly Leu Trp Ser Val
            260                 265                 270

ctc tgc ttc gtg tcc acc ttc gcc acc gtc tcc acc ttc ctt atc gac   864
Leu Cys Phe Val Ser Thr Phe Ala Thr Val Ser Thr Phe Leu Ile Asp
        275                 280                 285

atg gag cgc ttc aag tac ccg gag cgg ccc att atc ttc ctc tcg gcc   912
Met Glu Arg Phe Lys Tyr Pro Glu Arg Pro Ile Ile Phe Leu Ser Ala
    290                 295                 300

tgc tac ctc ttc gtg tcg gtg ggc tac cta gtg cgc ctg gtg gcg ggc   960
Cys Tyr Leu Phe Val Ser Val Gly Tyr Leu Val Arg Leu Val Ala Gly
305                 310                 315                 320
```

```
cac gag aag gtg gcg tgc agc ggt ggc gcg ccg ggc gcg ggg ggc gct   1008
His Glu Lys Val Ala Cys Ser Gly Gly Ala Pro Gly Ala Gly Gly Ala
                325                 330                 335

ggg ggc gcg ggc ggc gcg gcg gcg ggc gcg ggc gcg gcg ggc gcg ggc   1056
Gly Gly Ala Gly Gly Ala Ala Ala Gly Ala Gly Ala Ala Gly Ala Gly
            340                 345                 350

gcg ggc ggc ccg ggc ggg cgc ggc gag tac gag gag ctg ggc gcg gtg   1104
Ala Gly Gly Pro Gly Gly Arg Gly Glu Tyr Glu Glu Leu Gly Ala Val
        355                 360                 365

gag cag cac gtg cgc tac gag acc acc ggc ccc gcg ctg tgc acc gtg   1152
Glu Gln His Val Arg Tyr Glu Thr Thr Gly Pro Ala Leu Cys Thr Val
    370                 375                 380

gtc ttc ttg ctg gtc tac ttc ttc ggc atg gcc agc tcc atc tgg tgg   1200
Val Phe Leu Leu Val Tyr Phe Phe Gly Met Ala Ser Ser Ile Trp Trp
385                 390                 395                 400

gtg atc ttg tcg ctc aca tgg ttc ctg gcg gcc ggt atg aag tgg ggc   1248
Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly Met Lys Trp Gly
                405                 410                 415

aac gaa gcc atc gcc ggc tac tcg cag tac ttc cac ctg gcc gcg tgg   1296
Asn Glu Ala Ile Ala Gly Tyr Ser Gln Tyr Phe His Leu Ala Ala Trp
            420                 425                 430

ctt gtg ccc agc gtc aag tcc atc gcg gtg ctg gcg ctc agc tcg gtg   1344
Leu Val Pro Ser Val Lys Ser Ile Ala Val Leu Ala Leu Ser Ser Val
        435                 440                 445

gac ggc gac ccg gtg gcg ggc atc tgc tac gtg ggc aac cag agc ctg   1392
Asp Gly Asp Pro Val Ala Gly Ile Cys Tyr Val Gly Asn Gln Ser Leu
    450                 455                 460


gac aac ctg cgc ggc ttc gtg ctg gcg ccg ctg gtc atc tac ctc ttc   1440
Asp Asn Leu Arg Gly Phe Val Leu Ala Pro Leu Val Ile Tyr Leu Phe
465                 470                 475                 480

atc ggc acc atg ttc ctg ctg gcc ggc ttc gtg tcc ctc ttc cgc atc   1488
Ile Gly Thr Met Phe Leu Leu Ala Gly Phe Val Ser Leu Phe Arg Ile
                485                 490                 495

cgc tcg gtc atc aag caa cag gac ggc ccc acc aag acg cac aag ctg   1536
Arg Ser Val Ile Lys Gln Gln Asp Gly Pro Thr Lys Thr His Lys Leu
            500                 505                 510

gag aag ctg atg atc cgc ctg ggc ctg ttc acc gtg ctc tac acc gtg   1584
Glu Lys Leu Met Ile Arg Leu Gly Leu Phe Thr Val Leu Tyr Thr Val
        515                 520                 525

ccc gcc gcg gtg gtg gtc gcc tgc ctc ttc tac gag cag cac aac cgc   1632
Pro Ala Ala Val Val Val Ala Cys Leu Phe Tyr Glu Gln His Asn Arg
    530                 535                 540

ccg cgc tgg gag gcc acg cac aac tgc ccg tgc ctg cgg gac ctg cag   1680
Pro Arg Trp Glu Ala Thr His Asn Cys Pro Cys Leu Arg Asp Leu Gln
545                 550                 555                 560
```

```
ccc gac cag gca cgc agg ccc gac tac gcc gtc ttc atg ctc aag tac   1728
Pro Asp Gln Ala Arg Arg Pro Asp Tyr Ala Val Phe Met Leu Lys Tyr
                565                 570                 575

ttc atg tgc cta gtg gtg ggc atc acc tcg ggc gtg tgg gtc tgg tcc   1776
Phe Met Cys Leu Val Val Gly Ile Thr Ser Gly Val Trp Val Trp Ser
            580                 585                 590

ggc aag acg ctg gag tcc tgg cgc tcc ctg tgc acc cgc tgc tgc tgg   1824
Gly Lys Thr Leu Glu Ser Trp Arg Ser Leu Cys Thr Arg Cys Cys Trp
        595                 600                 605

gcc agc aag ggc gcc gcg gtg ggc ggg ggc gcg                       1857
Ala Ser Lys Gly Ala Ala Val Gly Gly Gly Ala
    610                 615
```

<210> 74
<211> 619
<212> PRT
<213> Homo sapiens

<400> 74

```
Ala Leu Ala Leu Leu Gln Arg Ser Ser Gly Ala Ala Ala Ala Ser Ala
 1               5                  10                  15
Lys Glu Leu Ala Cys Gln Glu Ile Thr Val Pro Leu Cys Lys Gly Ile
            20                  25                  30
Gly Tyr Asn Tyr Thr Tyr Met Pro Asn Gln Phe Asn His Asp Thr Gln
        35                  40                  45
Asp Glu Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile
    50                  55                  60
Gln Cys Ser Pro Asp Leu Lys Phe Phe Leu Cys Ser Met Tyr Thr Pro
65                  70                  75                  80
Ile Cys Leu Glu Asp Tyr Lys Lys Pro Leu Pro Pro Cys Arg Ser Val
                85                  90                  95
Cys Glu Arg Ala Lys Ala Gly Cys Ala Pro Leu Met Arg Gln Tyr Gly
            100                 105                 110

Phe Ala Trp Pro Asp Arg Met Arg Cys Asp Arg Leu Pro Glu Gln Gly
        115                 120                 125
Asn Pro Asp Thr Leu Cys Met Asp Tyr Asn Arg Thr Asp Leu Thr Thr
    130                 135                 140
Ala Ala Pro Ser Pro Pro Arg Arg Leu Pro Pro Pro Pro Pro Gly Glu
145                 150                 155                 160
Gln Pro Pro Ser Gly Ser Gly His Gly Arg Pro Pro Gly Ala Arg Pro
                165                 170                 175
Pro His Arg Gly Gly Gly Arg Gly Gly Gly Gly Gly Asp Ala Ala Ala
            180                 185                 190
Pro Pro Ala Arg Gly Gly Gly Gly Gly Gly Lys Ala Arg Pro Pro Gly
        195                 200                 205
Gly Gly Ala Ala Pro Cys Glu Pro Gly Cys Gln Cys Arg Ala Pro Met
    210                 215                 220
Val Ser Val Ser Ser Glu Arg His Pro Leu Tyr Asn Arg Val Lys Thr
225                 230                 235                 240
Gly Gln Ile Ala Asn Cys Ala Leu Pro Cys His Asn Pro Phe Phe Ser
                245                 250                 255
Gln Asp Glu Arg Ala Phe Thr Val Phe Trp Ile Gly Leu Trp Ser Val
            260                 265                 270
Leu Cys Phe Val Ser Thr Phe Ala Thr Val Ser Thr Phe Leu Ile Asp
        275                 280                 285
Met Glu Arg Phe Lys Tyr Pro Glu Arg Pro Ile Ile Phe Leu Ser Ala
    290                 295                 300
Cys Tyr Leu Phe Val Ser Val Gly Tyr Leu Val Arg Leu Val Ala Gly
```

```
305                 310                 315                 320
His Glu Lys Val Ala Cys Ser Gly Gly Ala Pro Gly Ala Gly Gly Ala
                325                 330                 335
Gly Gly Ala Gly Gly Ala Ala Ala Gly Ala Gly Ala Ala Gly Ala Gly
            340                 345                 350
Ala Gly Gly Pro Gly Gly Arg Gly Glu Tyr Glu Glu Leu Gly Ala Val
        355                 360                 365
Glu Gln His Val Arg Tyr Glu Thr Thr Gly Pro Ala Leu Cys Thr Val
    370                 375                 380
Val Phe Leu Leu Val Tyr Phe Phe Gly Met Ala Ser Ser Ile Trp Trp
385                 390                 395                 400
Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly Met Lys Trp Gly
                405                 410                 415
Asn Glu Ala Ile Ala Gly Tyr Ser Gln Tyr Phe His Leu Ala Ala Trp
            420                 425                 430
Leu Val Pro Ser Val Lys Ser Ile Ala Val Leu Ala Leu Ser Ser Val
        435                 440                 445
Asp Gly Asp Pro Val Ala Gly Ile Cys Tyr Val Gly Asn Gln Ser Leu
    450                 455                 460
Asp Asn Leu Arg Gly Phe Val Leu Ala Pro Leu Val Ile Tyr Leu Phe
465                 470                 475                 480
Ile Gly Thr Met Phe Leu Leu Ala Gly Phe Val Ser Leu Phe Arg Ile
                485                 490                 495
Arg Ser Val Ile Lys Gln Gln Asp Gly Pro Thr Lys Thr His Lys Leu
            500                 505                 510
Glu Lys Leu Met Ile Arg Leu Gly Leu Phe Thr Val Leu Tyr Thr Val
        515                 520                 525
Pro Ala Ala Val Val Val Ala Cys Leu Phe Tyr Glu Gln His Asn Arg
    530                 535                 540
Pro Arg Trp Glu Ala Thr His Asn Cys Pro Cys Leu Arg Asp Leu Gln
545                 550                 555                 560
Pro Asp Gln Ala Arg Arg Pro Asp Tyr Ala Val Phe Met Leu Lys Tyr
                565                 570                 575
Phe Met Cys Leu Val Val Gly Ile Thr Ser Gly Val Trp Val Trp Ser
            580                 585                 590
Gly Lys Thr Leu Glu Ser Trp Arg Ser Leu Cys Thr Arg Cys Cys Trp
        595                 600                 605
Ala Ser Lys Gly Ala Ala Val Gly Gly Gly Ala
    610                 615
```

<210> 75
<211> 966
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(966)

<400> 75

```
ctg gca agg agc agc aat cct ttt gag gag aag agg cac tct ggt ttt   48
Leu Ala Arg Ser Ser Asn Pro Phe Glu Glu Lys Arg His Ser Gly Phe
 1               5                  10                  15

ttg aat ttt cag ctt ttc tgc tct ggt ttc tcc cca tct ttg tgc tgt   96
Leu Asn Phe Gln Leu Phe Cys Ser Gly Phe Ser Pro Ser Leu Cys Cys
            20                  25                  30

cag aca ggg aca ttt agg tct gca gaa gtt ttc tat tgc ctt ttg ttc   144
Gln Thr Gly Thr Phe Arg Ser Ala Glu Val Phe Tyr Cys Leu Leu Phe
        35                  40                  45
```

```
agc tgt gcc ctg ctc aca gac cag aag gag aag atg gct tta cat ttt   192
Ser Cys Ala Leu Leu Thr Asp Gln Lys Glu Lys Met Ala Leu His Phe
     50                  55                  60

ctt ttc cat cag aca ctt caa ctc ata cat ttg gag ctg gaa aag atg   240
Leu Phe His Gln Thr Leu Gln Leu Ile His Leu Glu Leu Glu Lys Met
 65                  70                  75                  80

att tta aaa aat ctt ttc atg ccc tat tgg gat gtg tgg cat cat cag   288
Ile Leu Lys Asn Leu Phe Met Pro Tyr Trp Asp Val Trp His His Gln
                 85                  90                  95

ttt caa tat gca aat caa att ttg ggt aag ggt cta tac tgc ttc ttc   336
Phe Gln Tyr Ala Asn Gln Ile Leu Gly Lys Gly Leu Tyr Cys Phe Phe
            100                 105                 110

agg gta ttt gtt ttc tat tcc tgt agc ttt gtg gag ctt gca gtg agc   384
Arg Val Phe Val Phe Tyr Ser Cys Ser Phe Val Glu Leu Ala Val Ser
        115                 120                 125

cga gat cgt gcc act gca ctc cag cct ggg cga cag agc gag act ctg   432
Arg Asp Arg Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser Glu Thr Leu
    130                 135                 140

tct caa aaa aaa aaa aaa aga aat gca act gat ttt tgc atg ttg tct   480
Ser Gln Lys Lys Lys Lys Arg Asn Ala Thr Asp Phe Cys Met Leu Ser
145                 150                 155                 160

ttg tgt att gaa gga aca tac ctc caa ata ata aga gcc att tgt tgc   528
Leu Cys Ile Glu Gly Thr Tyr Leu Gln Ile Ile Arg Ala Ile Cys Cys
                165                 170                 175

aaa ccc aca gcc act ggc cca gtc cct ttc act cag tgt gtc acc aaa   576
Lys Pro Thr Ala Thr Gly Pro Val Pro Phe Thr Gln Cys Val Thr Lys
            180                 185                 190

ggc agc ttc aag gct caa tgg caa gag acc acc tat aac ctc ttc acc   624
Gly Ser Phe Lys Ala Gln Trp Gln Glu Thr Thr Tyr Asn Leu Phe Thr
        195                 200                 205

ttc tgc tgc ctc ttt ctg ctg cca ctg act gcc atg gtc atc tgc tat   672
Phe Cys Cys Leu Phe Leu Leu Pro Leu Thr Ala Met Val Ile Cys Tyr
    210                 215                 220

agc cgc att gtc ctc agt gtt ata ttt tct aaa ttc cta gcc cct gct   720
Ser Arg Ile Val Leu Ser Val Ile Phe Ser Lys Phe Leu Ala Pro Ala
225                 230                 235                 240

ggt gaa ttt gcc ctc ccc cgc tcc ttt gac aat tgt ccc cgt gtt cgt   768
Gly Glu Phe Ala Leu Pro Arg Ser Phe Asp Asn Cys Pro Arg Val Arg
                245                 250                 255

ctc cgg gcc ctg aga ctg gcc ctg ctt atc ttg ctg acc ttc atc ctc   816
Leu Arg Ala Leu Arg Leu Ala Leu Leu Ile Leu Leu Thr Phe Ile Leu
            260                 265                 270

tgc tgg aca cct tat tac cta ctg ggt atg tgg tac tgg ttc tcc ccc   864
Cys Trp Thr Pro Tyr Tyr Leu Leu Gly Met Trp Tyr Trp Phe Ser Pro
        275                 280                 285

acc atg cta act gaa gtc cct ccc agc ctg agc cac atc ctt ttc ctc   912
Thr Met Leu Thr Glu Val Pro Pro Ser Leu Ser His Ile Leu Phe Leu
    290                 295                 300
```

```
ttg ggc ctc ctc aat gct cct ttg gat cct ctc ctc tat ggg gcc ttc   960
Leu Gly Leu Leu Asn Ala Pro Leu Asp Pro Leu Leu Tyr Gly Ala Phe
305                 310                 315                 320

acc ctt                                                       966
Thr Leu
```

<210> 76
<211> 322
<212> PRT
<213> Homo sapiens

<400> 76

```
Leu Ala Arg Ser Ser Asn Pro Phe Glu Glu Lys Arg His Ser Gly Phe
 1               5                  10                  15
Leu Asn Phe Gln Leu Phe Cys Ser Gly Phe Ser Pro Ser Leu Cys Cys
            20                  25                  30
Gln Thr Gly Thr Phe Arg Ser Ala Glu Val Phe Tyr Cys Leu Leu Phe
        35                  40                  45
Ser Cys Ala Leu Leu Thr Asp Gln Lys Glu Lys Met Ala Leu His Phe
    50                  55                  60
Leu Phe His Gln Thr Leu Gln Leu Ile His Leu Glu Leu Glu Lys Met
65                  70                  75                  80
Ile Leu Lys Asn Leu Phe Met Pro Tyr Trp Asp Val Trp His His Gln
                85                  90                  95
Phe Gln Tyr Ala Asn Gln Ile Leu Gly Lys Gly Leu Tyr Cys Phe Phe
            100                 105                 110
Arg Val Phe Val Phe Tyr Ser Cys Ser Phe Val Glu Leu Ala Val Ser
        115                 120                 125
Arg Asp Arg Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser Glu Thr Leu
    130                 135                 140

Ser Gln Lys Lys Lys Lys Arg Asn Ala Thr Asp Phe Cys Met Leu Ser
145                 150                 155                 160
Leu Cys Ile Glu Gly Thr Tyr Leu Gln Ile Ile Arg Ala Ile Cys Cys
                165                 170                 175
Lys Pro Thr Ala Thr Gly Pro Val Pro Phe Thr Gln Cys Val Thr Lys
            180                 185                 190
Gly Ser Phe Lys Ala Gln Trp Gln Glu Thr Thr Tyr Asn Leu Phe Thr
        195                 200                 205
Phe Cys Cys Leu Phe Leu Leu Pro Leu Thr Ala Met Val Ile Cys Tyr
    210                 215                 220
Ser Arg Ile Val Leu Ser Val Ile Phe Ser Lys Phe Leu Ala Pro Ala
225                 230                 235                 240
Gly Glu Phe Ala Leu Pro Arg Ser Phe Asp Asn Cys Pro Arg Val Arg
                245                 250                 255
Leu Arg Ala Leu Arg Leu Ala Leu Leu Ile Leu Leu Thr Phe Ile Leu
            260                 265                 270
Cys Trp Thr Pro Tyr Tyr Leu Leu Gly Met Trp Tyr Trp Phe Ser Pro
        275                 280                 285
Thr Met Leu Thr Glu Val Pro Pro Ser Leu Ser His Ile Leu Phe Leu
    290                 295                 300
Leu Gly Leu Leu Asn Ala Pro Leu Asp Pro Leu Leu Tyr Gly Ala Phe
305                 310                 315                 320
Thr Leu
```

<210> 77
<211> 1212

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1212)

<400> 77

```
ctg ggc gca gtg act acg cct gta atc cca gca ctt ggg gac gcc gag   48
Leu Gly Ala Val Thr Thr Pro Val Ile Pro Ala Leu Gly Asp Ala Glu
 1               5                  10                  15

gca ggc agg tca tct gag gtc atc gtc ctg cat tac aac tac acc ggc   96
Ala Gly Arg Ser Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly
            20                  25                  30

aag ctc cgc ggt gcg cgc tac cag ccg ggt gcc ggc ctg cgc gcc gac   144
Lys Leu Arg Gly Ala Arg Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp
        35                  40                  45

gcc gtg gtg tgc ctg gcg gtg tgc gcc ttc atc gtg cta gag aat cta   192
Ala Val Val Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu
    50                  55                  60

gcc gtg ttg ttg gtg ctc gga cgc cac ccg cgc ttc cac gct ccc atg   240
Ala Val Leu Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met
65                  70                  75                  80

ttc ctg ctc ctg ggc agc ctc acg ttg tcg gat ctg ctg gca ggc gcc   288
Phe Leu Leu Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala
                85                  90                  95



gcc tac gcc gcc aac atc cta ctg tcg ggg ccg ctc acg ctg aaa ctg   336
Ala Tyr Ala Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu
            100                 105                 110

tcc ccc gcg ctc tgg ttc gca cgg gag gga ggc gtc ttc gtg gca ctc   384
Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu
        115                 120                 125

act gcg tcc gtg ctg agc ctc ctg gcc atc gcg ctg gag cgc agc ctc   432
Thr Ala Ser Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu
    130                 135                 140

acc atg gcg cgc agg ggg ccc gcg ccc gtc tcc agt cgg ggg cgc acg   480
Thr Met Ala Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr
145                 150                 155                 160

ctg gcg atg gca gcc gcg gcc tgg ggc gtg tcg ctg ctc ctc ggg ctc   528
Leu Ala Met Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu
                165                 170                 175

ctg cca gcg ctg ggc tgg aat tgc ctg ggt cgc ctg gac gct tgc tcc   576
Leu Pro Ala Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser
            180                 185                 190

act gtc ttg ccg ctc tac gcc aag gcc tac gtg ctc ttc tgc gtg ctc   624
Thr Val Leu Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu
        195                 200                 205

gcc ttc gtg ggc atc ctg gcc gct atc tgt gca ctc tac gcg cgc atc   672
```

```
Ala Phe Val Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile
    210                 215                 220

tac tgc cag gta cgc gcc aac gcg cgg cgc ctg ccg gca cgg ccc ggg   720
Tyr Cys Gln Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly
225                 230                 235                 240

act gcg ggg acc acc tcg acc cgg gcg cgt cgc aag ccg cgc tcg ctg   768
Thr Ala Gly Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu
                245                 250                 255

gcc ttg ctg cgc acg ctc agc gtg gtg ctc ctg gcc ttt gtg gca tgt   816
Ala Leu Leu Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys
            260                 265                 270

tgg ggc ccc ctc ttc ctg ctg ctg ttg ctc gac gtg gcg tgc ccg gcg   864
Trp Gly Pro Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala
        275                 280                 285

cgc acc tgt cct gta ctc ctg cag gcc gat ccc ttc ctg gga ctg gcc   912
Arg Thr Cys Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala
    290                 295                 300

atg gcc aac tca ctt ctg aac ccc atc atc tac acg ctc acc aac cgc   960
Met Ala Asn Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg
305                 310                 315                 320

gac ctg cgc cac gcg ctc ctg cgc ctg gtc tgc tgc gga cgc cac tcc   1008
Asp Leu Arg His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser
                325                 330                 335



tgc ggc aga gac ccg agt ggc tcc cag cag tcg gcg agc gcg gct gag   1056
Cys Gly Arg Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu
            340                 345                 350

gct tcc ggg ggc ctg cgc cgc tgc ctg ccc ccg ggc ctt gat ggg agc   1104
Ala Ser Gly Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser
        355                 360                 365

ttc agc ggc tcg gag cgc tca tcg ccc cag cgc gac ggg ctg gac acc   1152
Phe Ser Gly Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr
    370                 375                 380

agc ggc tcc aca ggc agc ccc gcc tgt gtg atg aaa tca tgt ctt tta   1200
Ser Gly Ser Thr Gly Ser Pro Ala Cys Val Met Lys Ser Cys Leu Leu
385                 390                 395                 400

gga aaa cat aag                                                   1212
Gly Lys His Lys
```

<210> 78
<211> 404
<212> PRT
<213> Homo sapiens

<400> 78

```
Leu Gly Ala Val Thr Thr Pro Val Ile Pro Ala Leu Gly Asp Ala Glu
 1               5                  10                  15
Ala Gly Arg Ser Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly
```

```
            20                  25                  30
Lys Leu Arg Gly Ala Arg Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp
        35                  40                  45
Ala Val Val Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu
    50                  55                  60
Ala Val Leu Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met
65                  70                  75                  80
Phe Leu Leu Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala
                85                  90                  95
Ala Tyr Ala Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu
            100                 105                 110
Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu
        115                 120                 125
Thr Ala Ser Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu
    130                 135                 140
Thr Met Ala Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr
145                 150                 155                 160
Leu Ala Met Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu
                165                 170                 175
Leu Pro Ala Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser
            180                 185                 190
Thr Val Leu Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu
        195                 200                 205
Ala Phe Val Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile
    210                 215                 220
Tyr Cys Gln Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly
225                 230                 235                 240
Thr Ala Gly Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu
                245                 250                 255
Ala Leu Leu Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys
            260                 265                 270

Trp Gly Pro Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala
        275                 280                 285
Arg Thr Cys Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala
    290                 295                 300
Met Ala Asn Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg
305                 310                 315                 320
Asp Leu Arg His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser
                325                 330                 335
Cys Gly Arg Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu
            340                 345                 350
Ala Ser Gly Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser
        355                 360                 365
Phe Ser Gly Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr
    370                 375                 380
Ser Gly Ser Thr Gly Ser Pro Ala Cys Val Met Lys Ser Cys Leu Leu
385                 390                 395                 400
Gly Lys His Lys
```

<210> 79
<211> 1113
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1113)

<400> 79
tct ccg cag gca cct ggg act tgg gct gct gcc tgg gtc ccc ctc ccc 48

```
Ser Pro Gln Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro
 1               5                  10                  15

acg gtt gat gtt cca gac cat gcc cac tat acc ctg ggc aca gtg atc   96
Thr Val Asp Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile
            20                  25                  30

ttg ctg gtg gga ctc acg ggg atg ctg ggc aac ctg acg gtc atc tat   144
Leu Leu Val Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr
        35                  40                  45

acc ttc tgc agg agc aga agc ctc cgg aca cct gcc aac atg ttc att   192
Thr Phe Cys Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile
    50                  55                  60

atc aac ctc gcg gtc agc gac ttc ctc atg tcc ttc acc cag gcc cct   240
Ile Asn Leu Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro
65                  70                  75                  80

gtc ttc ttc acc agt agc ctc tat aag cag tgg ctc ttt ggg gag aca   288
Val Phe Phe Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr
                85                  90                  95

ggc tgc gag ttc tat gcc ttc tgt gga gct ctc ttt ggc att tcc tcc   336
Gly Cys Glu Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser
            100                 105                 110

atg atc acc ctg acg gcc atc gcc ctg gac cgc tac ctg gta atc aca   384
Met Ile Thr Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr
        115                 120                 125

cgc ccg ctg gcc acc ttt ggt gtg gcg tcc aag agg cgt gcg gca ttt   432
Arg Pro Leu Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe
    130                 135                 140

gtc ctg ctg ggc gtt tgg ctc tat gcc ctg gcc tgg agt ctg cca ccc   480
Val Leu Leu Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro
145                 150                 155                 160

ttc ttc ggc tgg agc gcc tac gtg ccc gag ggg ttg ctg aca tcc tgc   528
Phe Phe Gly Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys
                165                 170                 175

tcc tgg gac tac atg agc ttc acg ccg gcc gtg cgt gcc tac acc atg   576
Ser Trp Asp Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met
            180                 185                 190

ctt ctc tgc tgc ttc gtg ttc ttc ctc cct ctg ctt atc atc atc tac   624
Leu Leu Cys Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr
        195                 200                 205

tgc tac atc ttc atc ttc agg gcc atc cgg gag aca gga cgg gct ctc   672
Cys Tyr Ile Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu
    210                 215                 220

cag acc ttc ggg gcc tgc aag ggc aat ggc gag tcc ctg tgg cag cgg   720
Gln Thr Phe Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg
225                 230                 235                 240

cag cgg ctg cag agc gag tgc aag atg gcc aag atc atg ctg ctg gtc   768
Gln Arg Leu Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val
                245                 250                 255
```

```
atc ctc ctc ttc gtg ctc tcc tgg gct ccc tat tcc gct gtg gcc ctg   816
Ile Leu Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu
            260                 265                 270

gtg gcc ttt gct ggg tac gca cac gtc ctg aca ccc tac atg agc tcg   864
Val Ala Phe Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser
        275                 280                 285

gtg cca gcc gtc atc gcc aag gcc tct gca atc cac aac ccc atc att   912
Val Pro Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile
    290                 295                 300

tac gcc atc acc cac ccc aag tac agg tca gat gct gtg gct tcc tgg   960
Tyr Ala Ile Thr His Pro Lys Tyr Arg Ser Asp Ala Val Ala Ser Trp
305                 310                 315                 320

cag tcc aga cgt ctt ggg gta cac ttg tac ccc tgg tcc ctg gtg ttc   1008
Gln Ser Arg Arg Leu Gly Val His Leu Tyr Pro Trp Ser Leu Val Phe
                325                 330                 335

tgc cac cct agc gag ttt gaa aac cac aac tgg agc acc agg gat gtt   1056
Cys His Pro Ser Glu Phe Glu Asn His Asn Trp Ser Thr Arg Asp Val
            340                 345                 350

gcc cca ggc cac ctg atg aca gaa atg gag act aga gtg ttg tct ata   1104
Ala Pro Gly His Leu Met Thr Glu Met Glu Thr Arg Val Leu Ser Ile
        355                 360                 365


cta agc caa                                                      1113
Leu Ser Gln
    370
```

<210> 80
<211> 371
<212> PRT
<213> Homo sapiens

<400> 80

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Ser Pro Gln Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro
 1               5                  10                  15
Thr Val Asp Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile
            20                  25                  30
Leu Leu Val Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr
        35                  40                  45
Thr Phe Cys Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile
    50                  55                  60
Ile Asn Leu Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro
65                  70                  75                  80
Val Phe Phe Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr
                85                  90                  95
Gly Cys Glu Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser
            100                 105                 110
Met Ile Thr Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr
        115                 120                 125
Arg Pro Leu Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe
    130                 135                 140
Val Leu Leu Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro
145                 150                 155                 160
Phe Phe Gly Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys
                165                 170                 175
```

```
Ser Trp Asp Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met
            180                 185                 190
Leu Leu Cys Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr
        195                 200                 205
Cys Tyr Ile Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu
    210                 215                 220
Gln Thr Phe Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg
225                 230                 235                 240
Gln Arg Leu Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val
                245                 250                 255
Ile Leu Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu
            260                 265                 270
Val Ala Phe Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser
        275                 280                 285
Val Pro Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile
    290                 295                 300
Tyr Ala Ile Thr His Pro Lys Tyr Arg Ser Asp Ala Val Ala Ser Trp
305                 310                 315                 320
Gln Ser Arg Arg Leu Gly Val His Leu Tyr Pro Trp Ser Leu Val Phe
                325                 330                 335
Cys His Pro Ser Glu Phe Glu Asn His Asn Trp Ser Thr Arg Asp Val
            340                 345                 350
Ala Pro Gly His Leu Met Thr Glu Met Glu Thr Arg Val Leu Ser Ile
        355                 360                 365
Leu Ser Gln
    370
```

<210> 81
<211> 1119
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1119)

<400> 81

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tct cta cta aaa ata caa aaa att agt cgg acg tgg tgg cgg gtg cct   48
Ser Leu Leu Lys Ile Gln Lys Ile Ser Arg Thr Trp Trp Arg Val Pro
 1               5                  10                  15

agc aca gat gtg agc tgc tta cct atg tgg gga gac ttc agg gct gtg   96
Ser Thr Asp Val Ser Cys Leu Pro Met Trp Gly Asp Phe Arg Ala Val
             20                  25                  30

agt agt gaa ctc gaa atc tta gtt tta acg att gga att ttt att ttt   144
Ser Ser Glu Leu Glu Ile Leu Val Leu Thr Ile Gly Ile Phe Ile Phe
         35                  40                  45

ttc ctt gta ggg att ctg tcc aca ttt gga aat gga tat gtc ctt tac   192
Phe Leu Val Gly Ile Leu Ser Thr Phe Gly Asn Gly Tyr Val Leu Tyr
     50                  55                  60

atg tct tct aga cga aag aag aag ctg aga ccc gct gaa ata atg act   240
Met Ser Ser Arg Arg Lys Lys Lys Leu Arg Pro Ala Glu Ile Met Thr
 65                  70                  75                  80

atc aat tta gca gtc tgt gat ctg ggg att tca gtt gta ggc aag ccg   288
Ile Asn Leu Ala Val Cys Asp Leu Gly Ile Ser Val Val Gly Lys Pro
                 85                  90                  95

ttc acc atc atc tct tgc ttt tgt cac cgc tgg gtg ttt ggc tgg atc   336
```

```
Phe Thr Ile Ile Ser Cys Phe Cys His Arg Trp Val Phe Gly Trp Ile
            100                 105                 110

ggc tgc cgc tgg tat gga tgg gct gga ttt ttc ttt ggc tgt gga agc   384
Gly Cys Arg Trp Tyr Gly Trp Ala Gly Phe Phe Phe Gly Cys Gly Ser
        115                 120                 125

ctt atc acc atg act gct gtc agc ctg gat cga tat ttg aaa atc tgc   432
Leu Ile Thr Met Thr Ala Val Ser Leu Asp Arg Tyr Leu Lys Ile Cys
    130                 135                 140

tat tta tct tat ggg gtt tgg ctg aaa aga aag cac gcc tac atc tgc   480
Tyr Leu Ser Tyr Gly Val Trp Leu Lys Arg Lys His Ala Tyr Ile Cys
145                 150                 155                 160

ctg gca gcc atc tgg gcc tat gct tcc ttc tgg acc acc atg ccc ttg   528
Leu Ala Ala Ile Trp Ala Tyr Ala Ser Phe Trp Thr Thr Met Pro Leu
                165                 170                 175

gta ggt ctg ggg gac tac gta cct gag ccc ttc gga acc tcg tgc acc   576
Val Gly Leu Gly Asp Tyr Val Pro Glu Pro Phe Gly Thr Ser Cys Thr
            180                 185                 190

ctg gac tgg tgg ctg gcc cag gcc tcg gta ggg ggc cag gtt ttc atc   624
Leu Asp Trp Trp Leu Ala Gln Ala Ser Val Gly Gly Gln Val Phe Ile
        195                 200                 205


ctg aac atc ctc ttc ttc tgc ctc ttg ctc cca acg gct gtg atc gtg   672
Leu Asn Ile Leu Phe Phe Cys Leu Leu Leu Pro Thr Ala Val Ile Val
    210                 215                 220

ttc tcc tac gta aag atc att gcc aag gtt aag tcc tct tcc aaa gaa   720
Phe Ser Tyr Val Lys Ile Ile Ala Lys Val Lys Ser Ser Ser Lys Glu
225                 230                 235                 240

gta gct cat ttc gac agt cgg atc cat agc agc cat gtg ctg gaa atg   768
Val Ala His Phe Asp Ser Arg Ile His Ser Ser His Val Leu Glu Met
                245                 250                 255

aaa ctg aca aag gta gcg atg ttg att tgt gct gga ttc ctg att gcc   816
Lys Leu Thr Lys Val Ala Met Leu Ile Cys Ala Gly Phe Leu Ile Ala
            260                 265                 270

tgg att cct tat gca gtg gtg tct gtg tgg tca gct ttt gga agg cca   864
Trp Ile Pro Tyr Ala Val Val Ser Val Trp Ser Ala Phe Gly Arg Pro
        275                 280                 285

gac tcc att ccc ata cag ctc tct gtg gtg cca acc cta ctt gca aaa   912
Asp Ser Ile Pro Ile Gln Leu Ser Val Val Pro Thr Leu Leu Ala Lys
    290                 295                 300

tct gca gcg atg tac aat ccc atc att tac caa caa aac ttc tca ata   960
Ser Ala Ala Met Tyr Asn Pro Ile Ile Tyr Gln Gln Asn Phe Ser Ile
305                 310                 315                 320

tca aat ttt cgt gat tcc cta gct cag agc tca gtc cct tgg att cag   1008
Ser Asn Phe Arg Asp Ser Leu Ala Gln Ser Ser Val Pro Trp Ile Gln
                325                 330                 335

tgc tgt tat tat cct caa gag agc agg gga cag cta gaa agg gtt gta   1056
Cys Cys Tyr Tyr Pro Gln Glu Ser Arg Gly Gln Leu Glu Arg Val Val
            340                 345                 350
```

```
gaa tcg aga gat ttt gtg agg atg tca gca gtt agc gca gat cta caa   1104
Glu Ser Arg Asp Phe Val Arg Met Ser Ala Val Ser Ala Asp Leu Gln
        355                 360                 365

aaa ttc cag agg aat                                             1119
Lys Phe Gln Arg Asn
    370
```

<210> 82
<211> 373
<212> PRT
<213> Homo sapiens

<400> 82

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Ser Leu Leu Lys Ile Gln Lys Ile Ser Arg Thr Trp Trp Arg Val Pro
 1               5                  10                  15
Ser Thr Asp Val Ser Cys Leu Pro Met Trp Gly Asp Phe Arg Ala Val
            20                  25                  30
Ser Ser Glu Leu Glu Ile Leu Val Leu Thr Ile Gly Ile Phe Ile Phe
        35                  40                  45
Phe Leu Val Gly Ile Leu Ser Thr Phe Gly Asn Gly Tyr Val Leu Tyr
    50                  55                  60
Met Ser Ser Arg Arg Lys Lys Lys Leu Arg Pro Ala Glu Ile Met Thr
65                  70                  75                  80

Ile Asn Leu Ala Val Cys Asp Leu Gly Ile Ser Val Val Gly Lys Pro
                85                  90                  95
Phe Thr Ile Ile Ser Cys Phe Cys His Arg Trp Val Phe Gly Trp Ile
            100                 105                 110
Gly Cys Arg Trp Tyr Gly Trp Ala Gly Phe Phe Phe Gly Cys Gly Ser
        115                 120                 125
Leu Ile Thr Met Thr Ala Val Ser Leu Asp Arg Tyr Leu Lys Ile Cys
    130                 135                 140
Tyr Leu Ser Tyr Gly Val Trp Leu Lys Arg Lys His Ala Tyr Ile Cys
145                 150                 155                 160
Leu Ala Ala Ile Trp Ala Tyr Ala Ser Phe Trp Thr Thr Met Pro Leu
                165                 170                 175
Val Gly Leu Gly Asp Tyr Val Pro Glu Pro Phe Gly Thr Ser Cys Thr
            180                 185                 190
Leu Asp Trp Trp Leu Ala Gln Ala Ser Val Gly Gly Gln Val Phe Ile
        195                 200                 205
Leu Asn Ile Leu Phe Phe Cys Leu Leu Leu Pro Thr Ala Val Ile Val
    210                 215                 220
Phe Ser Tyr Val Lys Ile Ile Ala Lys Val Lys Ser Ser Ser Lys Glu
225                 230                 235                 240
Val Ala His Phe Asp Ser Arg Ile His Ser Ser His Val Leu Glu Met
                245                 250                 255
Lys Leu Thr Lys Val Ala Met Leu Ile Cys Ala Gly Phe Leu Ile Ala
            260                 265                 270
Trp Ile Pro Tyr Ala Val Val Ser Val Trp Ser Ala Phe Gly Arg Pro
        275                 280                 285
Asp Ser Ile Pro Ile Gln Leu Ser Val Val Pro Thr Leu Leu Ala Lys
    290                 295                 300
Ser Ala Ala Met Tyr Asn Pro Ile Ile Tyr Gln Gln Asn Phe Ser Ile
305                 310                 315                 320
Ser Asn Phe Arg Asp Ser Leu Ala Gln Ser Ser Val Pro Trp Ile Gln
                325                 330                 335
Cys Cys Tyr Tyr Pro Gln Glu Ser Arg Gly Gln Leu Glu Arg Val Val
            340                 345                 350
Glu Ser Arg Asp Phe Val Arg Met Ser Ala Val Ser Ala Asp Leu Gln
        355                 360                 365
```

```
Lys Phe Gln Arg Asn
    370


<210> 83
<211> 1533
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1533)

<400> 83
atg agt gtt gtt ctg cag gat act cag acg tta aca ata gac tca aac   48
Met Ser Val Val Leu Gln Asp Thr Gln Thr Leu Thr Ile Asp Ser Asn
 1               5                  10                  15

att aac agc ctg ctc ata gtt gcc ctg ctg gta act ggg att aca ggc   96
Ile Asn Ser Leu Leu Ile Val Ala Leu Leu Val Thr Gly Ile Thr Gly
            20                  25                  30

atg cac cac cac gcc cgg cta att tta aaa tta ttt gta agt aaa agt   144
Met His His His Ala Arg Leu Ile Leu Lys Leu Phe Val Ser Lys Ser
        35                  40                  45

agc ata aac ttt gct gat ttc atc tct cag agc tcc tct gcc agt ccc   192
Ser Ile Asn Phe Ala Asp Phe Ile Ser Gln Ser Ser Ser Ala Ser Pro
    50                  55                  60

gga ggt gtt gat tac att ttg cat ggc agt aca gtc acc ttt cag cat   240
Gly Gly Val Asp Tyr Ile Leu His Gly Ser Thr Val Thr Phe Gln His
65                  70                  75                  80

ggg caa aac tta agt ttt ata aat atc tcc atc att gat gac aat gaa   288
Gly Gln Asn Leu Ser Phe Ile Asn Ile Ser Ile Ile Asp Asp Asn Glu
                85                  90                  95

agt gaa ttt gag gag ccc att gaa att cta ctc act gga gct act gga   336
Ser Glu Phe Glu Glu Pro Ile Glu Ile Leu Leu Thr Gly Ala Thr Gly
            100                 105                 110

gga gcg gtc ctt ggg cgc cac cta gtg agc aga atc ata ata gct aag   384
Gly Ala Val Leu Gly Arg His Leu Val Ser Arg Ile Ile Ile Ala Lys
        115                 120                 125

agt gac tct ccc ttt gga gtt ata agg ttt ctc aat caa agc aaa att   432
Ser Asp Ser Pro Phe Gly Val Ile Arg Phe Leu Asn Gln Ser Lys Ile
    130                 135                 140

tct att gct aat ccc aat tcc aca atg att tta tca ctg gtg ctg gag   480
Ser Ile Ala Asn Pro Asn Ser Thr Met Ile Leu Ser Leu Val Leu Glu
145                 150                 155                 160

cgg act gga gga ctc ttg gga gag att cag gtg aac tgg gag aca gta   528
Arg Thr Gly Gly Leu Leu Gly Glu Ile Gln Val Asn Trp Glu Thr Val
                165                 170                 175

gga ccc aac tct caa gaa gcc tta ctg cca cag aat aga gac att gca   576
Gly Pro Asn Ser Gln Glu Ala Leu Leu Pro Gln Asn Arg Asp Ile Ala
            180                 185                 190

gac cca gtg agc ggg ttg ttc tat ttt gga gaa gga gaa gga gga gtg   624
```

```
Asp Pro Val Ser Gly Leu Phe Tyr Phe Gly Glu Gly Glu Gly Gly Val
        195                 200                 205

aga acc ata att ctg aca atc tat cct cat gaa gaa att gaa gtt gaa   672
Arg Thr Ile Ile Leu Thr Ile Tyr Pro His Glu Glu Ile Glu Val Glu
    210                 215                 220

gag aca ttc att att aaa ctt cat ctt gtg aaa gga gaa gct aaa tta   720
Glu Thr Phe Ile Ile Lys Leu His Leu Val Lys Gly Glu Ala Lys Leu
225                 230                 235                 240

gac tcc aga gct aaa gat gtt aca tta acc ata caa gag ttt ggt gac   768
Asp Ser Arg Ala Lys Asp Val Thr Leu Thr Ile Gln Glu Phe Gly Asp
                245                 250                 255

cca aat gga gtt gtt cag ttt gct cct gaa act ttg tct aag aag act   816
Pro Asn Gly Val Val Gln Phe Ala Pro Glu Thr Leu Ser Lys Lys Thr
            260                 265                 270

tat tca gag cct ctg gct ctg gaa ggg ccc ctg ctc att acc ttc ttt   864
Tyr Ser Glu Pro Leu Ala Leu Glu Gly Pro Leu Leu Ile Thr Phe Phe
        275                 280                 285


gtc aga aga gtc aag ggc acc ttt gga gag att atg gtt tac tgg gaa   912
Val Arg Arg Val Lys Gly Thr Phe Gly Glu Ile Met Val Tyr Trp Glu
    290                 295                 300

tta agt agt gag ttt gac att act gaa gac ttt ctt tcc acc agt gga   960
Leu Ser Ser Glu Phe Asp Ile Thr Glu Asp Phe Leu Ser Thr Ser Gly
305                 310                 315                 320

ttt ttc acc att gct gat gga gag agt gaa gct agc ttt gat gtt cat  1008
Phe Phe Thr Ile Ala Asp Gly Glu Ser Glu Ala Ser Phe Asp Val His
                325                 330                 335

ttg cta cca gat gag gta cct gag ata gag gaa gat tat gtg atc cag  1056
Leu Leu Pro Asp Glu Val Pro Glu Ile Glu Glu Asp Tyr Val Ile Gln
            340                 345                 350

ctt gtt tct gta gag gga gga gcc gaa ctg gat ctg gag aag agt atc  1104
Leu Val Ser Val Glu Gly Gly Ala Glu Leu Asp Leu Glu Lys Ser Ile
        355                 360                 365

aca tgg ttc tct gtt tat gca aat gat gac cca cat gga gta ttt gcc  1152
Thr Trp Phe Ser Val Tyr Ala Asn Asp Asp Pro His Gly Val Phe Ala
    370                 375                 380

ctg tat tcg gat cgc cag tca ata ctt att ggg cag aac ctt att aga  1200
Leu Tyr Ser Asp Arg Gln Ser Ile Leu Ile Gly Gln Asn Leu Ile Arg
385                 390                 395                 400

tcc atc caa att aac ata acc cgg ctt gct gga aca ttt gga gat gtg  1248
Ser Ile Gln Ile Asn Ile Thr Arg Leu Ala Gly Thr Phe Gly Asp Val
                405                 410                 415

gct gtt ggg ctt cga ata tca tcg gat cat aaa gaa cag ccg att gtt  1296
Ala Val Gly Leu Arg Ile Ser Ser Asp His Lys Glu Gln Pro Ile Val
            420                 425                 430

acc gaa aat gca gag agg cag ctg gtg gtc aaa gat ggt gcc aca tat  1344
Thr Glu Asn Ala Glu Arg Gln Leu Val Val Lys Asp Gly Ala Thr Tyr
```

```
        435                 440                 445

aaa gtg gac gtg ttt gga acc ttt tat tac agc ttc atc tcc tgt act   1392
Lys Val Asp Val Phe Gly Thr Phe Tyr Tyr Ser Phe Ile Ser Cys Thr
    450                 455                 460

gat gga gct gta aat cta aca tac atc cag atc att tca aag cct att   1440
Asp Gly Ala Val Asn Leu Thr Tyr Ile Gln Ile Ile Ser Lys Pro Ile
465                 470                 475                 480

ttt tct cac tac aca gat gcc tat ata ttt ctt cat tac agc ctt tta   1488
Phe Ser His Tyr Thr Asp Ala Tyr Ile Phe Leu His Tyr Ser Leu Leu
                485                 490                 495

aat act ttt ctc tgt gat aat tcc cac ttt aaa att tcg aga aag       1533
Asn Thr Phe Leu Cys Asp Asn Ser His Phe Lys Ile Ser Arg Lys
            500                 505                 510
```

<210> 84
<211> 511
<212> PRT
<213> Homo sapiens

<400> 84

```
Met Ser Val Val Leu Gln Asp Thr Gln Thr Leu Thr Ile Asp Ser Asn
 1               5                  10                  15
Ile Asn Ser Leu Leu Ile Val Ala Leu Leu Val Thr Gly Ile Thr Gly
            20                  25                  30
Met His His His Ala Arg Leu Ile Leu Lys Leu Phe Val Ser Lys Ser
        35                  40                  45
Ser Ile Asn Phe Ala Asp Phe Ile Ser Gln Ser Ser Ser Ala Ser Pro
    50                  55                  60
Gly Gly Val Asp Tyr Ile Leu His Gly Ser Thr Val Thr Phe Gln His
65                  70                  75                  80
Gly Gln Asn Leu Ser Phe Ile Asn Ile Ser Ile Ile Asp Asp Asn Glu
                85                  90                  95
Ser Glu Phe Glu Glu Pro Ile Glu Ile Leu Leu Thr Gly Ala Thr Gly
            100                 105                 110
Gly Ala Val Leu Gly Arg His Leu Val Ser Arg Ile Ile Ile Ala Lys
        115                 120                 125
Ser Asp Ser Pro Phe Gly Val Ile Arg Phe Leu Asn Gln Ser Lys Ile
    130                 135                 140
Ser Ile Ala Asn Pro Asn Ser Thr Met Ile Leu Ser Leu Val Leu Glu
145                 150                 155                 160
Arg Thr Gly Gly Leu Leu Gly Glu Ile Gln Val Asn Trp Glu Thr Val
                165                 170                 175
Gly Pro Asn Ser Gln Glu Ala Leu Leu Pro Gln Asn Arg Asp Ile Ala
            180                 185                 190
Asp Pro Val Ser Gly Leu Phe Tyr Phe Gly Glu Gly Glu Gly Gly Val
        195                 200                 205
Arg Thr Ile Ile Leu Thr Ile Tyr Pro His Glu Glu Ile Glu Val Glu
    210                 215                 220
Glu Thr Phe Ile Ile Lys Leu His Leu Val Lys Gly Glu Ala Lys Leu
225                 230                 235                 240
Asp Ser Arg Ala Lys Asp Val Thr Leu Thr Ile Gln Glu Phe Gly Asp
                245                 250                 255
Pro Asn Gly Val Val Gln Phe Ala Pro Glu Thr Leu Ser Lys Lys Thr
            260                 265                 270
Tyr Ser Glu Pro Leu Ala Leu Glu Gly Pro Leu Leu Ile Thr Phe Phe
        275                 280                 285
Val Arg Arg Val Lys Gly Thr Phe Gly Glu Ile Met Val Tyr Trp Glu
```

```
    290                 295                 300
Leu Ser Ser Glu Phe Asp Ile Thr Glu Asp Phe Leu Ser Thr Ser Gly
305                 310                 315                 320
Phe Phe Thr Ile Ala Asp Gly Glu Ser Glu Ala Ser Phe Asp Val His
                325                 330                 335
Leu Leu Pro Asp Glu Val Pro Glu Ile Glu Glu Asp Tyr Val Ile Gln
            340                 345                 350
Leu Val Ser Val Glu Gly Gly Ala Glu Leu Asp Leu Glu Lys Ser Ile
        355                 360                 365
Thr Trp Phe Ser Val Tyr Ala Asn Asp Asp Pro His Gly Val Phe Ala
    370                 375                 380
Leu Tyr Ser Asp Arg Gln Ser Ile Leu Ile Gly Gln Asn Leu Ile Arg
385                 390                 395                 400
Ser Ile Gln Ile Asn Ile Thr Arg Leu Ala Gly Thr Phe Gly Asp Val
                405                 410                 415
Ala Val Gly Leu Arg Ile Ser Ser Asp His Lys Glu Gln Pro Ile Val
            420                 425                 430
Thr Glu Asn Ala Glu Arg Gln Leu Val Val Lys Asp Gly Ala Thr Tyr
        435                 440                 445
Lys Val Asp Val Phe Gly Thr Phe Tyr Tyr Ser Phe Ile Ser Cys Thr
    450                 455                 460
Asp Gly Ala Val Asn Leu Thr Tyr Ile Gln Ile Ile Ser Lys Pro Ile
465                 470                 475                 480

Phe Ser His Tyr Thr Asp Ala Tyr Ile Phe Leu His Tyr Ser Leu Leu
                485                 490                 495
Asn Thr Phe Leu Cys Asp Asn Ser His Phe Lys Ile Ser Arg Lys
            500                 505                 510
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<210> 85
<211> 2160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2160)

<400> 85

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ggg gga ggt att tta ttt atg ctg ctt ttc ccc tca aag atc cac cta   48
Gly Gly Gly Ile Leu Phe Met Leu Leu Phe Pro Ser Lys Ile His Leu
 1               5                  10                  15

atc acc tac aaa gtc tat ttc ttt ttc agg ttt aac ttt cag aga ttc   96
Ile Thr Tyr Lys Val Tyr Phe Phe Phe Arg Phe Asn Phe Gln Arg Phe
            20                  25                  30

cgc tgg atg aaa gcc atg atc cac atg atc aag gag att aat aag agg   144
Arg Trp Met Lys Ala Met Ile His Met Ile Lys Glu Ile Asn Lys Arg
        35                  40                  45

aag gat att ttg ccc aac atc act ctg ggc tat cag atc ttt gat acc   192
Lys Asp Ile Leu Pro Asn Ile Thr Leu Gly Tyr Gln Ile Phe Asp Thr
    50                  55                  60

tgt ttt acc atc tcc aaa tca gtg gaa gca gtc ttg gta ttt ctt aca   240
Cys Phe Thr Ile Ser Lys Ser Val Glu Ala Val Leu Val Phe Leu Thr
65                  70                  75                  80

ggg cag gaa gaa aac agg ccc aat ttt aga aac agc act gga gca ttt   288
Gly Gln Glu Glu Asn Arg Pro Asn Phe Arg Asn Ser Thr Gly Ala Phe
                85                  90                  95
```

```
ccg gca gga att gtt gga gca ggt gga tca ttc tta tca gtt cct gct   336
Pro Ala Gly Ile Val Gly Ala Gly Gly Ser Phe Leu Ser Val Pro Ala
            100                 105                 110

tca aga att cta ggg tta tat tat ttg cct cag gtg ggc tat acc tct   384
Ser Arg Ile Leu Gly Leu Tyr Tyr Leu Pro Gln Val Gly Tyr Thr Ser
        115                 120                 125

acc tgc gtg att ctt agt gac aaa tac cag ttt cca tct tat ctt cgt   432
Thr Cys Val Ile Leu Ser Asp Lys Tyr Gln Phe Pro Ser Tyr Leu Arg
    130                 135                 140

gta ata gcc agc gat aag atc cag tcg aag gct gtg gta aaa cgt atc   480
Val Ile Ala Ser Asp Lys Ile Gln Ser Lys Ala Val Val Lys Arg Ile
145                 150                 155                 160

caa cac ttt cac ttt ctc act ctg tcg ccc agg ctg gag tgc agt ggc   528
Gln His Phe His Phe Leu Thr Leu Ser Pro Arg Leu Glu Cys Ser Gly
                165                 170                 175


gcc atc ctg gct cat ggc aac ctc tgc ctc cca gta gct ggg att aca   576
Ala Ile Leu Ala His Gly Asn Leu Cys Leu Pro Val Ala Gly Ile Thr
            180                 185                 190

ggt gtg tgc cac cat gcc aga cta att ttt gta ttt tta gta gag aca   624
Gly Val Cys His His Ala Arg Leu Ile Phe Val Phe Leu Val Glu Thr
        195                 200                 205

ggg ttt tgc cat gtt gcc cag gct gac gga gtc tcg ctc tgt tgc cat   672
Gly Phe Cys His Val Ala Gln Ala Asp Gly Val Ser Leu Cys Cys His
    210                 215                 220

gct gga gta tac aat tct cct gcc tca gcc ccc cta gta gct ggg act   720
Ala Gly Val Tyr Asn Ser Pro Ala Ser Ala Pro Leu Val Ala Gly Thr
225                 230                 235                 240

aca ggc gca cac cac cac gct cag cta att ttt gta ttt tta aga tat   768
Thr Gly Ala His His His Ala Gln Leu Ile Phe Val Phe Leu Arg Tyr
                245                 250                 255

gta aca ctt ctg tca ttg cag aaa gga cag agc tgc cct aat gtg ttc   816
Val Thr Leu Leu Ser Leu Gln Lys Gly Gln Ser Cys Pro Asn Val Phe
            260                 265                 270

atg cat tat cta ggg gaa gaa tat ttc cag cac agg gaa cag cac ctt   864
Met His Tyr Leu Gly Glu Glu Tyr Phe Gln His Arg Glu Gln His Leu
        275                 280                 285

cta aac cct gag gcg cgt gtg gct ggc act ttg gag gaa cag aaa aga   912
Leu Asn Pro Glu Ala Arg Val Ala Gly Thr Leu Glu Glu Gln Lys Arg
    290                 295                 300

agt caa tgt ggc tgg aaa gac tta tct att gtg tat aca tac ttc tgt   960
Ser Gln Cys Gly Trp Lys Asp Leu Ser Ile Val Tyr Thr Tyr Phe Cys
305                 310                 315                 320

aat gtt atg tac cat aac cta gct cag aga ttg gta ata ttt tct atg   1008
Asn Val Met Tyr His Asn Leu Ala Gln Arg Leu Val Ile Phe Ser Met
                325                 330                 335
```

```
tta ttt aat tca gat tta ctc tgg aaa act caa cat atg aaa att ctg   1056
Leu Phe Asn Ser Asp Leu Leu Trp Lys Thr Gln His Met Lys Ile Leu
            340                 345                 350

att tct aaa ata aat ata aag gga aaa tat ttt tta ggc ttt caa gat   1104
Ile Ser Lys Ile Asn Ile Lys Gly Lys Tyr Phe Leu Gly Phe Gln Asp
        355                 360                 365

gat tct tgg aat cat agg tcc ttc aca agc agg aac aga cct ctt ccc   1152
Asp Ser Trp Asn His Arg Ser Phe Thr Ser Arg Asn Arg Pro Leu Pro
    370                 375                 380

cat tca gtg tgt act gat gtg tgt cct cct ggg act cgg aag ggg att   1200
His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Arg Lys Gly Ile
385                 390                 395                 400

cgt tca gag gga gaa cca ata tgc tgc ttt gac tcc atc cca tgt gct   1248
Arg Ser Glu Gly Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys Ala
                405                 410                 415


gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa tgt   1296
Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln Cys
            420                 425                 430

ggt gaa gac tat tgg tca aat gca caa aag agc gag tgt gtg ctg aaa   1344
Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu Lys
        435                 440                 445

gag gtg gaa tac ctt gct tat gat gag gcc ctg gga ttc aca ctt gtc   1392
Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu Val
    450                 455                 460

att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca gtc aca gct gtg   1440
Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala Val
465                 470                 475                 480

tat gtg ata cac agg cac act ccc ctg gtg aac gcc agt gac tgg cag   1488
Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp Gln
                485                 490                 495

ctg ggc ttt ctc att cag gtt tct ctg atc atc atg ctg ctg tcg tcc   1536
Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser Ser
            500                 505                 510

atg ctt ttc att gac aag cca cac aac tgg tcc tgc atg gct ggc cag   1584
Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly Gln
        515                 520                 525

gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct tgc ctt ctt gga   1632
Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu Gly
    530                 535                 540

aag act agt tca ctg ttt tta gcc tac aga att tcc aaa tcc aaa act   1680
Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys Thr
545                 550                 555                 560

caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc att gtg cta atc   1728
Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu Ile
                565                 570                 575

tct gtt cta gcg gag att ggc ata tgt aca gcc tac ttg ata ttg gaa   1776
```

```
Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu Glu
            580                 585                 590

cct ccc atg gta tac aag aac atg gaa tct caa aat aca aag atc att   1824
Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile Ile
        595                 600                 605

ctg gga tgc aat gaa att tcc ata gag ttt ttg tac tcg atg ttt gga   1872
Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe Gly
    610                 615                 620

att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca act ttt gtg gct   1920
Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val Ala
625                 630                 635                 640

cgc cag tta cca gat aat tac tat gaa gga aaa tgc atc acc ttt ggg   1968
Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe Gly
                645                 650                 655


atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc cct gtt tat ttg   2016
Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr Leu
            660                 665                 670

agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata ttt gca atc ttg   2064
Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile Leu
        675                 680                 685

gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct cct aag tgc ctc   2112
Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys Leu
    690                 695                 700

att att ttg ctg agg cca gag agg aac acc agt gaa att gtt tgt gga   2160
Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys Gly
705                 710                 715                 720


<210> 86
<211> 720
<212> PRT
<213> Homo sapiens

<400> 86
Gly Gly Gly Ile Leu Phe Met Leu Leu Phe Pro Ser Lys Ile His Leu
 1               5                  10                  15
Ile Thr Tyr Lys Val Tyr Phe Phe Phe Arg Phe Asn Phe Gln Arg Phe
            20                  25                  30
Arg Trp Met Lys Ala Met Ile His Met Ile Lys Glu Ile Asn Lys Arg
        35                  40                  45
Lys Asp Ile Leu Pro Asn Ile Thr Leu Gly Tyr Gln Ile Phe Asp Thr
    50                  55                  60
Cys Phe Thr Ile Ser Lys Ser Val Glu Ala Val Leu Val Phe Leu Thr
65                  70                  75                  80
Gly Gln Glu Glu Asn Arg Pro Asn Phe Arg Asn Ser Thr Gly Ala Phe
                85                  90                  95
Pro Ala Gly Ile Val Gly Ala Gly Gly Ser Phe Leu Ser Val Pro Ala
            100                 105                 110
Ser Arg Ile Leu Gly Leu Tyr Tyr Leu Pro Gln Val Gly Tyr Thr Ser
        115                 120                 125
Thr Cys Val Ile Leu Ser Asp Lys Tyr Gln Phe Pro Ser Tyr Leu Arg
    130                 135                 140
```

```
Val Ile Ala Ser Asp Lys Ile Gln Ser Lys Ala Val Val Lys Arg Ile
145                 150                 155                 160
Gln His Phe His Phe Leu Thr Leu Ser Pro Arg Leu Glu Cys Ser Gly
                165                 170                 175
Ala Ile Leu Ala His Gly Asn Leu Cys Leu Pro Val Ala Gly Ile Thr
            180                 185                 190
Gly Val Cys His His Ala Arg Leu Ile Phe Val Phe Leu Val Glu Thr
        195                 200                 205
Gly Phe Cys His Val Ala Gln Ala Asp Gly Val Ser Leu Cys Cys His
    210                 215                 220
Ala Gly Val Tyr Asn Ser Pro Ala Ser Ala Pro Leu Val Ala Gly Thr
225                 230                 235                 240
Thr Gly Ala His His His Ala Gln Leu Ile Phe Val Phe Leu Arg Tyr
                245                 250                 255
Val Thr Leu Leu Ser Leu Gln Lys Gly Gln Ser Cys Pro Asn Val Phe
            260                 265                 270
Met His Tyr Leu Gly Glu Glu Tyr Phe Gln His Arg Glu Gln His Leu
        275                 280                 285
Leu Asn Pro Glu Ala Arg Val Ala Gly Thr Leu Glu Glu Gln Lys Arg
    290                 295                 300
Ser Gln Cys Gly Trp Lys Asp Leu Ser Ile Val Tyr Thr Tyr Phe Cys
305                 310                 315                 320
Asn Val Met Tyr His Asn Leu Ala Gln Arg Leu Val Ile Phe Ser Met
                325                 330                 335
Leu Phe Asn Ser Asp Leu Leu Trp Lys Thr Gln His Met Lys Ile Leu
            340                 345                 350
Ile Ser Lys Ile Asn Ile Lys Gly Lys Tyr Phe Leu Gly Phe Gln Asp
        355                 360                 365
Asp Ser Trp Asn His Arg Ser Phe Thr Ser Arg Asn Arg Pro Leu Pro
    370                 375                 380
His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Arg Lys Gly Ile
385                 390                 395                 400
Arg Ser Glu Gly Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys Ala
                405                 410                 415
Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln Cys
            420                 425                 430
Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu Lys
        435                 440                 445
Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu Val
    450                 455                 460
Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala Val
465                 470                 475                 480
Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp Gln
                485                 490                 495
Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser Ser
            500                 505                 510
Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly Gln
        515                 520                 525
Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu Gly
    530                 535                 540
Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys Thr
545                 550                 555                 560
Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu Ile
                565                 570                 575
Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu Glu
            580                 585                 590
Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile Ile
        595                 600                 605
Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe Gly
    610                 615                 620
Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val Ala
625                 630                 635                 640
Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe Gly
```

```
                645                 650                 655
Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr Leu
            660                 665                 670
Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile Leu
        675                 680                 685
Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys Leu
    690                 695                 700
Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys Gly
705                 710                 715                 720
```

<210> 87
<211> 933
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(933)

<400> 87

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cgg ctg gtg ctg gcc gcg gtg gag aca acc gtg ctg gtg ctc atc ttt   48
Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe
 1               5                  10                  15

gca gtg tcg ctg ctg ggc aac gtg tgc gcc ctg gtg ctg gtg gcg cgc   96
Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg
            20                  25                  30

cga cga cgc cgc ggc gcg act gcc tgc ctg gta ctc aac ctc ttc tgc   144
Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys
        35                  40                  45

gcg gac ctg ctc ttc atc agc gct atc cct ctg gtg ctg gcc gtg cgc   192
Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg
    50                  55                  60

tgg act gag gcc tgg ctg ctg ggc ccc gtt gcc tgc cac ctg ctc ttc   240
Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe
65                  70                  75                  80

tac gtg atg acc ctg agc ggc agc gtc acc atc ctc acg ctg gcc gcg   288
Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala
                85                  90                  95

gtc agc ctg gag cgc atg gtg tgc atc gtg cac ctg cag cgc ggc gtg   336
Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val
            100                 105                 110

cgg ggt cct ggg cgg cgg gcg cgg gca gtg ctg ctg gcg ctc atc tgg   384
Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp
        115                 120                 125

ggc tat tcg gcg gtc gcc gct ctg cct ctc tgc gtc ttc ttc cga gtc   432
Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val
    130                 135                 140

gtc ccg caa cgg ctc ccc ggc gcc gac cag gtg agc gcc cct ctg tgt   480
Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Val Ser Ala Pro Leu Cys
145                 150                 155                 160

atc tcg tgg gat gtc tct ttt gtt act ttg aac ttc ttg gtg cca gga   528
Ile Ser Trp Asp Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly
```

```
                165                 170                 175

ctg gtc att gtg atc agt tac tcc aaa att tta cag atc cgc gtg tcc   576
Leu Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Arg Val Ser
            180                 185                 190

cag cag gac ttc cgg ctc ttc cgc acc ctc ttc ctc ctc atg gtc tcc   624
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
        195                 200                 205

ttc ttc atc atg tgg agc ccc atc atc atc acc atc ctc ctc atc ctg   672
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
    210                 215                 220

atc cag aac ttc aag caa gac ctg gtc atc tgg ccg tcc ctc ttc ttc   720
Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
225                 230                 235                 240

tgg gtg gtg gcc ttc aca ttt gct aat tca gcc cta aac ccc atc ctc   768
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
                245                 250                 255

tac aac atg aca ctc aga gtc ttc agg cac agg gtc ctg gag att agg   816
Tyr Asn Met Thr Leu Arg Val Phe Arg His Arg Val Leu Glu Ile Arg
            260                 265                 270

gac aaa ctt tgg ccc ctg aca att ttg cat aag ttc agc tct ggc aca   864
Asp Lys Leu Trp Pro Leu Thr Ile Leu His Lys Phe Ser Ser Gly Thr
        275                 280                 285

agt cta cca ttg gga cat aca cac aca cag gca cac aca cac aca cat   912
Ser Leu Pro Leu Gly His Thr His Thr Gln Ala His Thr His Thr His
    290                 295                 300

gca cac aca cac ttg cac aca                                      933
Ala His Thr His Leu His Thr
305                 310
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<210> 88
<211> 311
<212> PRT
<213> Homo sapiens

<400> 88

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Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe
 1               5                  10                  15
Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg
            20                  25                  30
Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys
        35                  40                  45
Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg
    50                  55                  60
Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe
65                  70                  75                  80
Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala
                85                  90                  95
Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val
            100                 105                 110
Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp
        115                 120                 125
Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val
```

```
    130                 135                 140
Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Val Ser Ala Pro Leu Cys
145                 150                 155                 160
Ile Ser Trp Asp Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly
                165                 170                 175
Leu Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Arg Val Ser
            180                 185                 190
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
        195                 200                 205
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
    210                 215                 220
Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
225                 230                 235                 240
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
                245                 250                 255
Tyr Asn Met Thr Leu Arg Val Phe Arg His Arg Val Leu Glu Ile Arg
            260                 265                 270

Asp Lys Leu Trp Pro Leu Thr Ile Leu His Lys Phe Ser Ser Gly Thr
        275                 280                 285
Ser Leu Pro Leu Gly His Thr His Thr Gln Ala His Thr His Thr His
    290                 295                 300
Ala His Thr His Leu His Thr
305                 310
```

<210> 89
<211> 1059
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1059)

<400> 89

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atg gga agt gga att agt tca gag agc aag gag tca gcc aaa aga tca   48
Met Gly Ser Gly Ile Ser Ser Glu Ser Lys Glu Ser Ala Lys Arg Ser
 1               5                  10                  15

aaa gaa ctg gag aaa aag ctt cag gag gat gct gag cga gat gca aga   96
Lys Glu Leu Glu Lys Lys Leu Gln Glu Asp Ala Glu Arg Asp Ala Arg
            20                  25                  30

acc gta aag ctg cta cta tta gga gca gga gaa tct ggg aaa agt act  144
Thr Val Lys Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr
        35                  40                  45

att gtt aaa caa atg aag aga ata ata cag gga aaa cat tat aca tcg  192
Ile Val Lys Gln Met Lys Arg Ile Ile Gln Gly Lys His Tyr Thr Ser
    50                  55                  60

gag gaa tct gct gca tgg agc ttg agt gcc tgg tcg aac ata cac aaa  240
Glu Glu Ser Ala Ala Trp Ser Leu Ser Ala Trp Ser Asn Ile His Lys
65                  70                  75                  80

tca ata aac tta atc cat cac ata aac aga acc aag aac aaa aac cac  288
Ser Ile Asn Leu Ile His His Ile Asn Arg Thr Lys Asn Lys Asn His
                85                  90                  95

atg att agc tca ata gaa gca gaa aag gcc ttc cac aaa att caa cag  336
Met Ile Ser Ser Ile Glu Ala Glu Lys Ala Phe His Lys Ile Gln Gln
            100                 105                 110
```

```
cct ttg atg cta aaa act ctc aat aaa caa gag aga gag acg ata agt   384
Pro Leu Met Leu Lys Thr Leu Asn Lys Gln Glu Arg Glu Thr Ile Ser
        115                 120                 125

aat cta tgg tca ggg gtt aat atc caa aat tta tat tca tac acc gaa   432
Asn Leu Trp Ser Gly Val Asn Ile Gln Asn Leu Tyr Ser Tyr Thr Glu
    130                 135                 140

tat tta ata cca gcc tgc aca aca agc tac ctt aat gat tta gat aga   480
Tyr Leu Ile Pro Ala Cys Thr Thr Ser Tyr Leu Asn Asp Leu Asp Arg
145                 150                 155                 160

ata aca gca tct ggg tat gtg cca aat gaa caa gat gtt ctc cat tct   528
Ile Thr Ala Ser Gly Tyr Val Pro Asn Glu Gln Asp Val Leu His Ser
                165                 170                 175

cga gtg aaa acg act gga atc att gaa act caa ttc tcc ttt aaa gac   576
Arg Val Lys Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp
            180                 185                 190

ttg cac ttc agg atg ttt gat gta ggt gga cag aga tct gag aga aag   624
Leu His Phe Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys
        195                 200                 205

aag tgg att cac tgc ttt gaa gga gtt aca tgc att ata ttt tgt gct   672
Lys Trp Ile His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Cys Ala
    210                 215                 220

gca ctt agt gcc tat gac atg gtc ctc gtg gaa gac gaa gaa gtg aat   720
Ala Leu Ser Ala Tyr Asp Met Val Leu Val Glu Asp Glu Glu Val Asn
225                 230                 235                 240

aga atg cat gaa agc ctt cac ctg ttc aac agt atc tgt aat cac aag   768
Arg Met His Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His Lys
                245                 250                 255

tat ttt tca aca acc tcc att gtc ctg ttc ctc aac aaa aaa gat atc   816
Tyr Phe Ser Thr Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp Ile
            260                 265                 270

ttt caa gaa aag gta acc aag gtg cat ctt agt atc tgc ttt cca gaa   864
Phe Gln Glu Lys Val Thr Lys Val His Leu Ser Ile Cys Phe Pro Glu
        275                 280                 285

tac act ggg cca aat aca ttt gaa gat gca gga aac tac atc aag aac   912
Tyr Thr Gly Pro Asn Thr Phe Glu Asp Ala Gly Asn Tyr Ile Lys Asn
    290                 295                 300

cag ttt cta gac ctg aat tta aaa aaa gaa gat aag gaa att tat tcc   960
Gln Phe Leu Asp Leu Asn Leu Lys Lys Glu Asp Lys Glu Ile Tyr Ser
305                 310                 315                 320

cac atg acc tgt gct act gac acc caa aat gtc aag ttt gtg ttt gac  1008
His Met Thr Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe Asp
                325                 330                 335

gca gtt aca gat ata ata atc aaa gag aat cta aaa gac tgt ggg ctt  1056
Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly Leu
            340                 345                 350

ttc                                                             1059
Phe
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<210> 90
<211> 353
<212> PRT
<213> Homo sapiens

<400> 90
Met Gly Ser Gly Ile Ser Ser Glu Ser Lys Glu Ser Ala Lys Arg Ser
1 5 10 15
Lys Glu Leu Glu Lys Lys Leu Gln Glu Asp Ala Glu Arg Asp Ala Arg
20 25 30
Thr Val Lys Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr
35 40 45

Ile Val Lys Gln Met Lys Arg Ile Ile Gln Gly Lys His Tyr Thr Ser
50 55 60
Glu Glu Ser Ala Ala Trp Ser Leu Ser Ala Trp Ser Asn Ile His Lys
65 70 75 80
Ser Ile Asn Leu Ile His His Ile Asn Arg Thr Lys Asn Lys Asn His
85 90 95
Met Ile Ser Ser Ile Glu Ala Glu Lys Ala Phe His Lys Ile Gln Gln
100 105 110
Pro Leu Met Leu Lys Thr Leu Asn Lys Gln Glu Arg Glu Thr Ile Ser
115 120 125
Asn Leu Trp Ser Gly Val Asn Ile Gln Asn Leu Tyr Ser Tyr Thr Glu
130 135 140
Tyr Leu Ile Pro Ala Cys Thr Thr Ser Tyr Leu Asn Asp Leu Asp Arg
145 150 155 160
Ile Thr Ala Ser Gly Tyr Val Pro Asn Glu Gln Asp Val Leu His Ser
165 170 175
Arg Val Lys Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp
180 185 190
Leu His Phe Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys
195 200 205
Lys Trp Ile His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Cys Ala
210 215 220
Ala Leu Ser Ala Tyr Asp Met Val Leu Val Glu Asp Glu Glu Val Asn
225 230 235 240
Arg Met His Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His Lys
245 250 255
Tyr Phe Ser Thr Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp Ile
260 265 270
Phe Gln Glu Lys Val Thr Lys Val His Leu Ser Ile Cys Phe Pro Glu
275 280 285
Tyr Thr Gly Pro Asn Thr Phe Glu Asp Ala Gly Asn Tyr Ile Lys Asn
290 295 300
Gln Phe Leu Asp Leu Asn Leu Lys Lys Glu Asp Lys Glu Ile Tyr Ser
305 310 315 320
His Met Thr Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe Asp
325 330 335
Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly Leu
340 345 350
Phe

<210> 91
<211> 960
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)...(960)

<400> 91

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tcg ccg gga tcc cgg gtg att ctg tac ata gtg ttt ggc ttt ggg gct   48
Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala
 1               5                  10                  15

gtg ctg gct gtg ttt gga aac ctc ctg gtg atg att tca atc ctc cat   96
Val Leu Ala Val Phe Gly Asn Leu Leu Val Met Ile Ser Ile Leu His
            20                  25                  30



ttc aag cag ctg cac tct ccg acc aat ttt ctc gtt gcc tct ctg gcc   144
Phe Lys Gln Leu His Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala
        35                  40                  45

tgc gct gat ttc ttg gtg ggt gtg act gtg atg ccc ttc agc atg gtc   192
Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Met Val
    50                  55                  60

agg acg gtg gag agc tgc tgg tat ttt ggg agg agt ttt tgt act ttc   240
Arg Thr Val Glu Ser Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe
65                  70                  75                  80

cac acc tgc tgt gat gtg gca ttt tgt tac tct tct ctc ttt cac ttg   288
His Thr Cys Cys Asp Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu
                85                  90                  95

tgc ttc atc tcc atc gac agg tac att gcg gtt act gac ccc ctg gtc   336
Cys Phe Ile Ser Ile Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val
            100                 105                 110

tat cct acc aag ttc acc gta tct gtg tca gga att tgc atc agc gtg   384
Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val
        115                 120                 125

tcc tgg atc ctg ccc ctc atg tac agc ggt gct gtg ttc tac aca ggt   432
Ser Trp Ile Leu Pro Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly
    130                 135                 140

gtc tat gac gat ggg ctg gag gaa tta tct gat gcc cta aac tgt ata   480
Val Tyr Asp Asp Gly Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile
145                 150                 155                 160

gga ggt tgt cag acc gtt gta aat caa aac tgg gtg ttg aca gat ttt   528
Gly Gly Cys Gln Thr Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe
                165                 170                 175

cta tcc ttc ttt ata cct acc ttt att atg ata att ctg tat ggt aac   576
Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn
            180                 185                 190

ata ttt ctt gtg gct aga cga cag gcg aaa aag ata gaa aat act gag   624
Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Glu
        195                 200                 205

aga aaa gca gct aaa acc ctg ggg gtc aca gtg gta gca ttt atg att   672
Arg Lys Ala Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile
    210                 215                 220

tca tgg tta cca tat agc att gat tca tta att gat gcc ttt atg ggc   720
```

```
Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly
225                 230                 235                 240

ttt ata acc cct gcc tgt att tat gag att tgc tgt tgg tgt gct tat   768
Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr
                245                 250                 255

tat aac tca gcc atg aat cct ttg att tat gct tta ttt tac cca tgg   816
Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp
            260                 265                 270



ttt agg aaa gca ata aaa aaa ctg aga aag tgc aaa gtg ttt agg gaa   864
Phe Arg Lys Ala Ile Lys Lys Leu Arg Lys Cys Lys Val Phe Arg Glu
        275                 280                 285

tat gaa aat aaa aca act agg ctg ggc gtg gtg ggt cac gcc tgt aat   912
Tyr Glu Asn Lys Thr Thr Arg Leu Gly Val Val Gly His Ala Cys Asn
    290                 295                 300

ccc agc act ttg gga ggc caa ggc ggg tgg atc aca agg tca aaa gat   960
Pro Ser Thr Leu Gly Gly Gln Gly Gly Trp Ile Thr Arg Ser Lys Asp
305                 310                 315                 320
```

<210> 92
<211> 320
<212> PRT
<213> Homo sapiens

<400> 92

```
Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala
 1               5                  10                  15
Val Leu Ala Val Phe Gly Asn Leu Leu Val Met Ile Ser Ile Leu His
            20                  25                  30
Phe Lys Gln Leu His Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala
        35                  40                  45
Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Met Val
    50                  55                  60
Arg Thr Val Glu Ser Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe
65                  70                  75                  80
His Thr Cys Cys Asp Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu
                85                  90                  95
Cys Phe Ile Ser Ile Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val
            100                 105                 110
Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val
        115                 120                 125
Ser Trp Ile Leu Pro Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly
    130                 135                 140
Val Tyr Asp Asp Gly Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile
145                 150                 155                 160
Gly Gly Cys Gln Thr Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe
                165                 170                 175
Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn
            180                 185                 190
Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Glu
        195                 200                 205
Arg Lys Ala Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile
    210                 215                 220
Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly
225                 230                 235                 240
```

```
Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr
                245                 250                 255
Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp
            260                 265                 270
Phe Arg Lys Ala Ile Lys Lys Leu Arg Lys Cys Lys Val Phe Arg Glu
        275                 280                 285
Tyr Glu Asn Lys Thr Thr Arg Leu Gly Val Val Gly His Ala Cys Asn
    290                 295                 300
Pro Ser Thr Leu Gly Gly Gln Gly Gly Trp Ile Thr Arg Ser Lys Asp
305                 310                 315                 320
```

<210> 93
<211> 912
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(912)

<400> 93

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tgc tac aat cag acc ctg agc ttc acg gtg ctg acg tgc atc att tcc   48
Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile Ser
 1               5                  10                  15

ctt gtc gga ctg aca gga aac gcg gtt gtg ctc tgg ctc ctg ggc tac   96
Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Tyr
            20                  25                  30

cgc atg cgc agg aac gct gtc tcc atc tac atc ctc aac ctg gcc gca   144
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala Ala
        35                  40                  45

gca gac ttc ctc ttc ctc agc ttc cag att ata cgt ttg cca tta cgc   192
Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Leu Pro Leu Arg
    50                  55                  60

ctc atc aat atc agc cat ctc atc cgc aaa atc ctc gtt tct gtg atg   240
Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val Met
65                  70                  75                  80

acc ttt ccc tac ttt aca ggc ctg agt atg ctg agc gcc atc agc acc   288
Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
                85                  90                  95

gag cgc tgc ctg tct gtt ctg tgg ccc atc tgg tac cgc tgc cgc cgc   336
Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg
            100                 105                 110

ccc aca cac ctg tca gcg gtc gtg tgt gtc ctg ctc tgg ggc ctg tcc   384
Pro Thr His Leu Ser Ala Val Val Cys Val Leu Leu Trp Gly Leu Ser
        115                 120                 125

ctg ctg ttt agt atg ctg gag tgg agg ttc tgt gac ttc ctg ttt agt   432
Leu Leu Phe Ser Met Leu Glu Trp Arg Phe Cys Asp Phe Leu Phe Ser
    130                 135                 140

ggt gct gat tct agt tgg tgt gaa acg tca gat ttc atc cca gtc gcg   480
Gly Ala Asp Ser Ser Trp Cys Glu Thr Ser Asp Phe Ile Pro Val Ala
145                 150                 155                 160

tgg ctg att ttt tta tgt gtg gtt ctc tgt gtt tcc agc ctg gtc ctg   528
```

```
Trp Leu Ile Phe Leu Cys Val Val Leu Cys Val Ser Ser Leu Val Leu
                165                 170                 175

ctg gtc agg atc ctc tgt gga tcc cgg aag atg ccg ctg acc agg ctg   576
Leu Val Arg Ile Leu Cys Gly Ser Arg Lys Met Pro Leu Thr Arg Leu
            180                 185                 190

tac gtg acc atc ctg ctc aca gtg ctg gtc ttc ctc ctc tgc ggc ctg   624
Tyr Val Thr Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu
        195                 200                 205

ccc ttc ggc att ctg ggg gcc cta att tac agg atg cac ctg aat ttg   672
Pro Phe Gly Ile Leu Gly Ala Leu Ile Tyr Arg Met His Leu Asn Leu
    210                 215                 220

gaa gtc tta tat tgt cat gtt tat ctg gtt tgc atg tcc ctg tcc tct   720
Glu Val Leu Tyr Cys His Val Tyr Leu Val Cys Met Ser Leu Ser Ser
225                 230                 235                 240

cta aac agt agt gcc aac ccc atc att tac ttc ttc gtg ggc tcc ttt   768
Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
                245                 250                 255

agg cag cgt caa aat agg cag aac ctg aag ctg gtt ctc cag agg gct   816
Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys Leu Val Leu Gln Arg Ala
            260                 265                 270

ctg cag gac aag cct gag gtg gat aaa gca tct gca acg agg agc cgg   864
Leu Gln Asp Lys Pro Glu Val Asp Lys Ala Ser Ala Thr Arg Ser Arg
        275                 280                 285             -

acg aga acc acc tca acc tca tcc gcg tca acg cca cca agg cct acg   912
Thr Arg Thr Thr Ser Thr Ser Ser Ala Ser Thr Pro Pro Arg Pro Thr
    290                 295                 300
```

<210> 94
<211> 304
<212> PRT
<213> Homo sapiens

<400> 94

```
Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile Ser
 1               5                  10                  15
Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Tyr
            20                  25                  30
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala Ala
        35                  40                  45
Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Leu Pro Leu Arg
    50                  55                  60
Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val Met
65                  70                  75                  80
Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
                85                  90                  95
Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg
            100                 105                 110
Pro Thr His Leu Ser Ala Val Val Cys Val Leu Leu Trp Gly Leu Ser
        115                 120                 125
Leu Leu Phe Ser Met Leu Glu Trp Arg Phe Cys Asp Phe Leu Phe Ser
    130                 135                 140
Gly Ala Asp Ser Ser Trp Cys Glu Thr Ser Asp Phe Ile Pro Val Ala
145                 150                 155                 160
```

```
Trp Leu Ile Phe Leu Cys Val Val Leu Cys Val Ser Ser Leu Val Leu
                165                 170                 175
Leu Val Arg Ile Leu Cys Gly Ser Arg Lys Met Pro Leu Thr Arg Leu
            180                 185                 190
Tyr Val Thr Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu
        195                 200                 205
Pro Phe Gly Ile Leu Gly Ala Leu Ile Tyr Arg Met His Leu Asn Leu
    210                 215                 220
Glu Val Leu Tyr Cys His Val Tyr Leu Val Cys Met Ser Leu Ser Ser
225                 230                 235                 240
Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
                245                 250                 255
Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys Leu Val Leu Gln Arg Ala
            260                 265                 270
Leu Gln Asp Lys Pro Glu Val Asp Lys Ala Ser Ala Thr Arg Ser Arg
        275                 280                 285
Thr Arg Thr Thr Ser Thr Ser Ser Ala Ser Thr Pro Pro Arg Pro Thr
    290                 295                 300


<210> 95
<211> 921
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(921)

<400> 95
tgt ggc aag gag acc ctg atc ccg gtc ttc ctg atc ctt ttc att gcc   48
Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala
 1               5                  10                  15

ctg gtc ggg ctg gta gga aac ggg ttt gtg ctc tgg ctc ctg ggc ttc   96
Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe
            20                  25                  30

cgc atg cgc agg aac gcc ttc tct gtc tac gtc ctc agc ctg gcc ggg   144
Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly
        35                  40                  45

gcc gac ttc ctc ttc ctc tgc ttc cag att ata aat tgc ctg gtg tac   192
Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr
    50                  55                  60

ctc agt aac ttc ttc tgt tcc atc tcc atc aat ttc cct agc ttc ttc   240
Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe
65                  70                  75                  80

acc act gtg atg acc tgt gcc tac ctt gca ggc ctg agc atg ctg agc   288
Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser
                85                  90                  95

acc gtc agc acc gag cgc tgc ctg tcc gtc ctg tgg ccc atc tgg tat   336
Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
            100                 105                 110

cgc tgc cgc cgc ccc aga cac ctg tca gcg gtc gtg tgt gtc ctg ctc   384
Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu
        115                 120                 125

tgg gcc ctg tcc cta ctg ctg agc atc ttg gaa ggg aag ttc tgt ggc   432
```

```
Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly
    130                 135                 140

ttc tta ttt agt gat ggt gac tct ggt tgg tgt cag aca ttt gat ttc   480
Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe
145                 150                 155                 160


atc act gca gcg tgg ctg att ttt tta ttc atg gtt ctc tgt ggg tcc   528
Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser
                165                 170                 175

agt ctg gcc ctg ctg gtc agg atc ctc tgt ggc tcc agg ggt ctg cca   576
Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro
            180                 185                 190

ctg acc agg ctg tac ctg acc atc ctg ctc aca gtg ctg gtg ttc ctc   624
Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Phe Leu
        195                 200                 205

ctc tgc ggc ctg ccc ttt ggc att cag tgg ttc cta ata tta tgg atc   672
Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile
    210                 215                 220

tgg aag gat tct gat gtc tta ttt tgt cat att cat cca gtt tca gtt   720
Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val
225                 230                 235                 240

gtc ctg tca tct ctt aac agc agt gcc aac ccc atc att tac ttc ttc   768
Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe
                245                 250                 255

gtg ggc tct ttt agg aag cag gag tgc tca ctc tcc tgt tta agc aag   816
Val Gly Ser Phe Arg Lys Gln Glu Cys Ser Leu Ser Cys Leu Ser Lys
            260                 265                 270

cag aag tct ccc acc ctc ctt tca gag aga gac ttc tgg att gca gtt   864
Gln Lys Ser Pro Thr Leu Leu Ser Glu Arg Asp Phe Trp Ile Ala Val
        275                 280                 285

att gct gaa gta agc cga gga aga aga cac gag ggg ttc aca ctt tcc   912
Ile Ala Glu Val Ser Arg Gly Arg Arg His Glu Gly Phe Thr Leu Ser
    290                 295                 300

ttt tta ggc                                                      921
Phe Leu Gly
305


<210> 96
<211> 307
<212> PRT
<213> Homo sapiens

<400> 96
Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala
 1               5                  10                  15
Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe
            20                  25                  30
Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly
        35                  40                  45
Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr
```

```
    50                  55                  60
Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe
65                  70                  75                  80
Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser
                85                  90                  95
Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
            100                 105                 110

Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu
        115                 120                 125
Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly
    130                 135                 140
Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe
145                 150                 155                 160
Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser
                165                 170                 175
Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro
            180                 185                 190
Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Phe Leu
        195                 200                 205
Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile
    210                 215                 220
Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val
225                 230                 235                 240
Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe
                245                 250                 255
Val Gly Ser Phe Arg Lys Gln Glu Cys Ser Leu Ser Cys Leu Ser Lys
            260                 265                 270
Gln Lys Ser Pro Thr Leu Leu Ser Glu Arg Asp Phe Trp Ile Ala Val
        275                 280                 285
Ile Ala Glu Val Ser Arg Gly Arg Arg His Glu Gly Phe Thr Leu Ser
    290                 295                 300
Phe Leu Gly
305
```

<210> 97
<211> 912
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(912)

<400> 97

```
tgc tac aag cag acc ctg agc ttc acg ggg ctg acg tgc atc gtt tcc   48
Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly Leu Thr Cys Ile Val Ser
 1               5                  10                  15

ctt gtc gcg ctg aca gga aac gcg gtt gtg ctc tgg ctc ctg ggc tgc   96
Leu Val Ala Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Cys
            20                  25                  30

cgc atg cgc agg aac gct gtc tcc atc tac atc ctc aac ctg gtc gcg   144
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Val Ala
        35                  40                  45

gcc gac ttc ctc ttc ctt agc ggc cac att ata tgt tcg ccg tta cgc   192
Ala Asp Phe Leu Phe Leu Ser Gly His Ile Ile Cys Ser Pro Leu Arg
    50                  55                  60

ctc atc aat atc cgc cat ccc atc tcc aaa atc ctc agt cct gtg atg   240
```

```
Leu Ile Asn Ile Arg His Pro Ile Ser Lys Ile Leu Ser Pro Val Met
 65                  70                  75                  80

acc ttt ccc tac ttt ata ggc cta agc atg ctg agc gcc atc agc acc   288
Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
                85                  90                  95

gag cgc tgc ctg tcc atc ctg tgg ccc atc tgg tac cac tgc cgc cgc   336
Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile Trp Tyr His Cys Arg Arg
            100                 105                 110

ccc aga tac ctg tca tca gtc atg tgt gtc ctg ctc tgg gcc ctg tcc   384
Pro Arg Tyr Leu Ser Ser Val Met Cys Val Leu Leu Trp Ala Leu Ser
        115                 120                 125

ctg ctg cgg agt atc ctg gag tgg atg ttc tgt gac ttc ctg ttt agt   432
Leu Leu Arg Ser Ile Leu Glu Trp Met Phe Cys Asp Phe Leu Phe Ser
    130                 135                 140

ggt gct aat tct gtt tgg tgt gaa acg tca gat ttc att aca atc gcg   480
Gly Ala Asn Ser Val Trp Cys Glu Thr Ser Asp Phe Ile Thr Ile Ala
145                 150                 155                 160

tgg ctg gtt ttt tta tgt gtg gtt ctc tgt ggg tcc agc ctg gtc ctg   528
Trp Leu Val Phe Leu Cys Val Val Leu Cys Gly Ser Ser Leu Val Leu
                165                 170                 175

ctg gtc agg att ctc tgt gga tcc cgg aag atg ccg ctg acc agg ctg   576
Leu Val Arg Ile Leu Cys Gly Ser Arg Lys Met Pro Leu Thr Arg Leu
            180         -       185                 190

tac gtg acc atc ctc ctc aca gtg ctg gtc ttc ctc ctc tgt ggc ctg   624
Tyr Val Thr Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu
        195                 200                 205

ccc ttt ggc att cag tgg gcc ctg ttt tcc agg atc cac ctg gat tgg   672
Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser Arg Ile His Leu Asp Trp
    210                 215                 220

aaa gtc tta ttt tgt cat gtg cat cta gtt tcc att ttc ctg tcc gct   720
Lys Val Leu Phe Cys His Val His Leu Val Ser Ile Phe Leu Ser Ala
225                 230                 235                 240

ctt aac agc agt gcc aac ccc atc att tac ttc ttc gtg ggc tcc ttt   768
Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
                245                 250                 255

agg cag cgt caa aat agg cag aac ctg aag ctg gac agc atg tgc agg   816
Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys Leu Asp Ser Met Cys Arg
            260                 265                 270

aga acg gcc ctt tat aaa acc atc aga tct cgt gag agt tat tca cta   864
Arg Thr Ala Leu Tyr Lys Thr Ile Arg Ser Arg Glu Ser Tyr Ser Leu
        275                 280                 285

tca cga gaa cag cag agg gaa gac cca acc cat gat tca ata ctt tcc   912
Ser Arg Glu Gln Gln Arg Glu Asp Pro Thr His Asp Ser Ile Leu Ser
    290                 295                 300
```

<210> 98
<211> 304

<212> PRT
<213> Homo sapiens

<400> 98
Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly Leu Thr Cys Ile Val Ser
1 5 10 15
Leu Val Ala Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Cys
20 25 30
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Val Ala
35 40 45
Ala Asp Phe Leu Phe Leu Ser Gly His Ile Ile Cys Ser Pro Leu Arg
50 55 60
Leu Ile Asn Ile Arg His Pro Ile Ser Lys Ile Leu Ser Pro Val Met
65 70 75 80
Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
85 90 95
Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile Trp Tyr His Cys Arg Arg
100 105 110
Pro Arg Tyr Leu Ser Ser Val Met Cys Val Leu Leu Trp Ala Leu Ser
115 120 125
Leu Leu Arg Ser Ile Leu Glu Trp Met Phe Cys Asp Phe Leu Phe Ser
130 135 140
Gly Ala Asn Ser Val Trp Cys Glu Thr Ser Asp Phe Ile Thr Ile Ala
145 150 155 160
Trp Leu Val Phe Leu Cys Val Val Leu Cys Gly Ser Ser Leu Val Leu
165 170 175
Leu Val Arg Ile Leu Cys Gly Ser Arg Lys Met Pro Leu Thr Arg Leu
180 185 190
Tyr Val Thr Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu
195 200 205
Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser Arg Ile His Leu Asp Trp
210 215 220
Lys Val Leu Phe Cys His Val His Leu Val Ser Ile Phe Leu Ser Ala
225 230 235 240
Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
245 250 255
Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys Leu Asp Ser Met Cys Arg
260 265 270
Arg Thr Ala Leu Tyr Lys Thr Ile Arg Ser Arg Glu Ser Tyr Ser Leu
275 280 285
Ser Arg Glu Gln Gln Arg Glu Asp Pro Thr His Asp Ser Ile Leu Ser
290 295 300

<210> 99
<211> 975
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(975)

<400> 99
cac agc ccc acc cac acc ttc ctc ttc ttt ctg gtc ctg gcc atc ttt 48
His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu Ala Ile Phe
1 5 10 15

tca gtg gcc ttc atg gga aac tct gtc atg gtt ctc ctc atc tac ctg 96
Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu Ile Tyr Leu
20 25 30

gac acc cag ctc cac acc ccc atg tac ttc ctc ctc agt caa ctg ttc 144

```
Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Phe
         35                  40                  45


ctc atg gac ctc atg ctc atc tgc tct acc gta ccc aag atg gcc ttc   192
Leu Met Asp Leu Met Leu Ile Cys Ser Thr Val Pro Lys Met Ala Phe
     50                  55                  60

aac tac ttg tct ggc agc aag tcc att tct atg gct ggt tgt gcc aca   240
Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Ala Thr
 65                  70                  75                  80

caa att ttc ttc tat gta tca ctg ctt ggc tcc gaa tgc ttt ctg ttg   288
Gln Ile Phe Phe Tyr Val Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu
                 85                  90                  95

gct gtt atg tct tat gac cgc tat att gcc att tgc cac cct cta aga   336
Ala Val Met Ser Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
            100                 105                 110

tac acc aat ctc atg aga ccc aaa att tgt gga ctt atg act gcc ttc   384
Tyr Thr Asn Leu Met Arg Pro Lys Ile Cys Gly Leu Met Thr Ala Phe
        115                 120                 125

tcc tgg atc ctg ggc tct atg gat gca atc att gat gct gta gcg aca   432
Ser Trp Ile Leu Gly Ser Met Asp Ala Ile Ile Asp Ala Val Ala Thr
    130                 135                 140

ttt tcc ttc tcc tac tgt ggg tct cgg gaa ata gcc cac ttc ttc-tgt   480
Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
145                 150                 155                 160

gac ttc cct tcc cta cta atc ctc tca tgc aat gac aca tca ata ttt   528
Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe
                165                 170                 175

gaa aag gtt ctt ttc atc tgc tgt ata gta atg att gtt ttt cct gtt   576
Glu Lys Val Leu Phe Ile Cys Cys Ile Val Met Ile Val Phe Pro Val
            180                 185                 190

gca atc atc atc gct tcc tat gct cga gtt att ctg gct gtc att cac   624
Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His
        195                 200                 205

atg gga tct gga gag ggt cgt cgc aaa gct ttt act acc tgt tcc tct   672
Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser
    210                 215                 220

cac ctc atg gtg gtg gga atg tac tat gga gca ggt ttg ttc atg tac   720
His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Gly Leu Phe Met Tyr
225                 230                 235                 240

ata cgg ccc aca tct gat cgc tcc cct atg cag gac aag ctg gtg tct   768
Ile Arg Pro Thr Ser Asp Arg Ser Pro Met Gln Asp Lys Leu Val Ser
                245                 250                 255

gta ttc tac acc atc ctc act ccc atg ctg aat ccc ctc atc tac agc   816
Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser
            260                 265                 270

ctc cgc aac aag gag gtg acc aga gca ctc agg aaa gtg aga gga gcc   864
Leu Arg Asn Lys Glu Val Thr Arg Ala Leu Arg Lys Val Arg Gly Ala
```

275 280 285

```
ccg ctg gaa agg aaa cat tcg gac tcc ggt ttc agc acc tcc tcc aga   912
Pro Leu Glu Arg Lys His Ser Asp Ser Gly Phe Ser Thr Ser Ser Arg
    290                 295                 300

agc aca gga tgt gcg acc ttc agc ctt tgt gcc cac ctc cga gcc acc   960
Ser Thr Gly Cys Ala Thr Phe Ser Leu Cys Ala His Leu Arg Ala Thr
305                 310                 315                 320

agc tcc gca gaa gta                                               975
Ser Ser Ala Glu Val
                325
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<210> 100
<211> 325
<212> PRT
<213> Homo sapiens

<400> 100

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His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu Ala Ile Phe
 1               5                  10                  15
Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu Ile Tyr Leu
            20                  25                  30
Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Phe
        35                  40                  45
Leu Met Asp Leu Met Leu Ile Cys Ser Thr Val Pro Lys Met Ala Phe
    50                  55                  60
Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Ala Thr
65                  70                  75                  80
Gln Ile Phe Phe Tyr Val Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu
                85                  90                  95
Ala Val Met Ser Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
            100                 105                 110
Tyr Thr Asn Leu Met Arg Pro Lys Ile Cys Gly Leu Met Thr Ala Phe
        115                 120                 125
Ser Trp Ile Leu Gly Ser Met Asp Ala Ile Ile Asp Ala Val Ala Thr
    130                 135                 140
Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
145                 150                 155                 160
Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe
                165                 170                 175
Glu Lys Val Leu Phe Ile Cys Cys Ile Val Met Ile Val Phe Pro Val
            180                 185                 190
Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His
        195                 200                 205
Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser
    210                 215                 220
His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Gly Leu Phe Met Tyr
225                 230                 235                 240
Ile Arg Pro Thr Ser Asp Arg Ser Pro Met Gln Asp Lys Leu Val Ser
                245                 250                 255
Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser
            260                 265                 270
Leu Arg Asn Lys Glu Val Thr Arg Ala Leu Arg Lys Val Arg Gly Ala
        275                 280                 285
Pro Leu Glu Arg Lys His Ser Asp Ser Gly Phe Ser Thr Ser Ser Arg
    290                 295                 300
Ser Thr Gly Cys Ala Thr Phe Ser Leu Cys Ala His Leu Arg Ala Thr
305                 310                 315                 320
```

```
Ser Ser Ala Glu Val
                325


<210> 101
<211> 927
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(927)

<400> 101
cga tgg gaa ctt caa att ttc ttc ttt gtg aca ttt tcc ctg atc tac   48
Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser Leu Ile Tyr
 1               5                  10                  15

ggt gct act gtg atg gga aac att ctc att atg gtc aca gtg aca tgt   96
Gly Ala Thr Val Met Gly Asn Ile Leu Ile Met Val Thr Val Thr Cys
            20                  25                  30

agg tca acc ctt cat tct ccc ttg tac ttt ctc ctt gga aat ctc tct   144
Arg Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly Asn Leu Ser
        35                  40                  45

ttt ttg gac atg tgt ctc tcc act gcc aca aca ccc aag atg atc ata   192
Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys Met Ile Ile
    50                  55                  60

gat ttg ctc act gac cac aag acc atc tct gtg tgg ggc tgc gtg acc   240
Asp Leu Leu Thr Asp His Lys Thr Ile Ser Val Trp Gly Cys Val Thr
65                  70                  75                  80

cag atg ttc ttc atg cac ttc ttt ggg ggt gct gag atg act ctt ctg   288
Gln Met Phe Phe Met His Phe Phe Gly Gly Ala Glu Met Thr Leu Leu
                85                  90                  95

ata atc atg gcc ttt gac agg tat gta gcc ata tgt aaa ccc ctg cac   336
Ile Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
            100                 105                 110

tat agg aca atc atg agc cac aag ctg cta aag ggg ttt gcg ata ctt   384
Tyr Arg Thr Ile Met Ser His Lys Leu Leu Lys Gly Phe Ala Ile Leu
        115                 120                 125

tca tgg ata att ggt ttt tta cac tcc ata agc cag ata gtt tta aca   432
Ser Trp Ile Ile Gly Phe Leu His Ser Ile Ser Gln Ile Val Leu Thr
    130                 135                 140

atg aac ttg cct ttc tgt ggc cac aat ctt gct tgc att gaa aca tac   480
Met Asn Leu Pro Phe Cys Gly His Asn Leu Ala Cys Ile Glu Thr Tyr
145                 150                 155                 160

acc ctg gaa tta ttt gtc att gct gac agc ggg ctg ctc tct ttc acc   528
Thr Leu Glu Leu Phe Val Ile Ala Asp Ser Gly Leu Leu Ser Phe Thr
                165                 170                 175

tgt ttc atc ctc ttg ctt gtt tct tac att gtc atc ctg gtc agt gta   576
Cys Phe Ile Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Val Ser Val
            180                 185                 190

cca aaa aaa tca tca cat ggg ctc tcc aag gcg ctg tcc aca ttg tct   624
```

```
Pro Lys Lys Ser Ser His Gly Leu Ser Lys Ala Leu Ser Thr Leu Ser
        195                 200                 205

gcc cac atc att gtg gtc act ctg ttc ttt gga cct tgt att ttt atc   672
Ala His Ile Ile Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe Ile
    210                 215                 220

tat gtt tgg cca ttc agt agt ttg gca agc aat aaa act ctt gcc gta   720
Tyr Val Trp Pro Phe Ser Ser Leu Ala Ser Asn Lys Thr Leu Ala Val
225                 230                 235                 240

ttt tat aca gtt atc aca ccc tta ctg aat ccg agt att tat acc ctg   768
Phe Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Ser Ile Tyr Thr Leu
                245                 250                 255

aga aat aag aaa atg caa gag gcc ata aga aaa tta cgg ttc caa tat   816
Arg Asn Lys Lys Met Gln Glu Ala Ile Arg Lys Leu Arg Phe Gln Tyr
            260                 265                 270

aat agt tca ccc agc aaa act ttc cct cag aca cga aga aga gat aaa   864
Asn Ser Ser Pro Ser Lys Thr Phe Pro Gln Thr Arg Arg Arg Asp Lys
        275                 280                 285

gac tat ccc aga aaa aca aga gct aag gaa ttt cat tac cac caa atc   912
Asp Tyr Pro Arg Lys Thr Arg Ala Lys Glu Phe His Tyr His Gln Ile
    290                 295                 300

ttt ttt ata aga aac                                              927
Phe Phe Ile Arg Asn
305
```

<210> 102
<211> 309
<212> PRT
<213> Homo sapiens

<400> 102

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Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser Leu Ile Tyr
 1               5                  10                  15
Gly Ala Thr Val Met Gly Asn Ile Leu Ile Met Val Thr Val Thr Cys
            20                  25                  30
Arg Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly Asn Leu Ser
        35                  40                  45
Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys Met Ile Ile
    50                  55                  60
Asp Leu Leu Thr Asp His Lys Thr Ile Ser Val Trp Gly Cys Val Thr
65                  70                  75                  80
Gln Met Phe Phe Met His Phe Phe Gly Gly Ala Glu Met Thr Leu Leu
                85                  90                  95
Ile Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
            100                 105                 110
Tyr Arg Thr Ile Met Ser His Lys Leu Leu Lys Gly Phe Ala Ile Leu
        115                 120                 125
Ser Trp Ile Ile Gly Phe Leu His Ser Ile Ser Gln Ile Val Leu Thr
    130                 135                 140
Met Asn Leu Pro Phe Cys Gly His Asn Leu Ala Cys Ile Glu Thr Tyr
145                 150                 155                 160
Thr Leu Glu Leu Phe Val Ile Ala Asp Ser Gly Leu Leu Ser Phe Thr
                165                 170                 175
Cys Phe Ile Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Val Ser Val
            180                 185                 190
Pro Lys Lys Ser Ser His Gly Leu Ser Lys Ala Leu Ser Thr Leu Ser
```

```
        195                 200                 205

Ala His Ile Ile Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe Ile
    210                 215                 220
Tyr Val Trp Pro Phe Ser Ser Leu Ala Ser Asn Lys Thr Leu Ala Val
225                 230                 235                 240
Phe Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Ser Ile Tyr Thr Leu
                245                 250                 255
Arg Asn Lys Lys Met Gln Glu Ala Ile Arg Lys Leu Arg Phe Gln Tyr
            260                 265                 270
Asn Ser Ser Pro Ser Lys Thr Phe Pro Gln Thr Arg Arg Arg Asp Lys
        275                 280                 285
Asp Tyr Pro Arg Lys Thr Arg Ala Lys Glu Phe His Tyr His Gln Ile
    290                 295                 300
Phe Phe Ile Arg Asn
305


<210> 103
<211> 930
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(930)

<400> 103
tct caa gat att cag ctc ttg gtc ttt gtg ctg atc tta att ttc tac   48
Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu Ile Phe Tyr
 1               5                  10                  15

ctt atc atc ctc cct gga aat ttt ctc att att ttc acc ata agg tca   96
Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr Ile Arg Ser
            20                  25                  30

gac cct ggg ctc aca gcc ccc ctc tat tta ttt ctg ggc aac ttg gcc   144
Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly Asn Leu Ala
        35                  40                  45

ttc ctg gat gca tcc tac tcc ttc att gtg gct ccc agg atg ttg gtg   192
Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg Met Leu Val
    50                  55                  60

gac ttc ctc tct gag aaa aag gta atc tcc tac aga ggc tgc atc act   240
Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly Cys Ile Thr
65                  70                  75                  80

cag ctc ttt ttc ttg cac ttc ctt gga gga ggg gag gga tta ctc ctt   288
Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly Leu Leu Leu
                85                  90                  95

gtt gtg atg gcc ttt gac cgc tac atc gcc atc tgc cgg cct ctg cac   336
Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg Pro Leu His
            100                 105                 110

tgt tca act gtc atg aac cct aga gcc tgc tat gca atg atg ttg gct   384
Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met Met Leu Ala
        115                 120                 125

ctg tgg ctt ggg ggt ttt gtc cac tcc att atc cag gtg gtc ctc atc   432
Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val Val Leu Ile
    130                 135                 140
```

```
ctc cgc ttg cct ttt tgt ggc cca aac cag ctg gac aac ttc ttc tgt   480
Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn Phe Phe Cys
145                 150                 155                 160

gat gtc cga cag ctt cta atg gtc ttc aac agt ggc ctg atg aca ctc   528
Asp Val Arg Gln Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
                165                 170                 175

ctg tgc ttt ctg ggg ctt ctg gct tcc tat gca gtc atc ctc tgc cat   576
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
            180                 185                 190

gtt cgt agg gca gct tct gaa ggg aag aac aag gcc atg tcc acg tgc   624
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
        195                 200                 205

acc act cgt gtc att att ata ctt ctt atg ttt gga cct gct atc ttc   672
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
    210                 215                 220

atc tac atg tgc cct ttc agg gcc tta cca gct gac aag atg gtt tct   720
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
225                 230                 235                 240

ctc ttt cac aca gtg atc ttt cca ttg atg aat cct atg att tat acc   768
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
                245                 250                 255

ctt cgc aac cag gaa gtg aaa act tcc atg aag agg tta ttg att cgt   816
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ile Arg
            260                 265                 270

tgt ctt gtg ctg tgc cga tta atg aca cag act cac aca cgg agt ggg   864
Cys Leu Val Leu Cys Arg Leu Met Thr Gln Thr His Thr Arg Ser Gly
        275                 280                 285

tta agg aac aga aag ttt att agg caa gaa gga aga gaa gag ctt ccc   912
Leu Arg Asn Arg Lys Phe Ile Arg Gln Glu Gly Arg Glu Glu Leu Pro
    290                 295                 300

cat aca gag gga gaa gca                                          930
His Thr Glu Gly Glu Ala
305                 310
```

<210> 104
<211> 310
<212> PRT
<213> Homo sapiens

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<400> 104
Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu Ile Phe Tyr
 1               5                  10                  15
Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr Ile Arg Ser
            20                  25                  30
Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly Asn Leu Ala
        35                  40                  45
Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg Met Leu Val
    50                  55                  60
Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly Cys Ile Thr
65                  70                  75                  80
```

```
Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly Leu Leu Leu
                85                  90                  95
Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg Pro Leu His
            100                 105                 110
Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met Met Leu Ala
        115                 120                 125
Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val Val Leu Ile
    130                 135                 140
Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn Phe Phe Cys
145                 150                 155                 160
Asp Val Arg Gln Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
                165                 170                 175
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
            180                 185                 190
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
        195                 200                 205
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
    210                 215                 220
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
225                 230                 235                 240
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
                245                 250                 255
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ile Arg
            260                 265                 270
Cys Leu Val Leu Cys Arg Leu Met Thr Gln Thr His Thr Arg Ser Gly
        275                 280                 285
Leu Arg Asn Arg Lys Phe Ile Arg Gln Glu Gly Arg Glu Glu Leu Pro
    290                 295                 300
His Thr Glu Gly Glu Ala
305                 310
```

<210> 105
<211> 972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(972)

<400> 105

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ttg gaa gct gct cac atc tgg atc tcc atc ccc ttt tgt gtg gtc tac   48
Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro Phe Cys Val Val Tyr
 1               5                  10                  15

ctg ttg gcc cta ctg gga aac ggc tct ctt ctg ttt atc atc aag aca   96
Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu Phe Ile Ile Lys Thr
            20                  25                  30

gag ccc agc ctc cat gag cca atg tac ctc ttc cta tgc atg ctg gct   144
Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe Leu Cys Met Leu Ala
        35                  40                  45

gta gtt gat ctt gtt gtg tgt tct aca gct gtg ccc aaa ctt ctc agt   192
Val Val Asp Leu Val Val Cys Ser Thr Ala Val Pro Lys Leu Leu Ser
    50                  55                  60

ctc ttc tgg ttc cat gat gga gag att cgc ttt gaa acc tgc ctc tca   240
Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe Glu Thr Cys Leu Ser
65                  70                  75                  80

ctc gtg ttc ctg att cac tct tgc tcc acc atg gaa tct ggc ttc ttc   288
```

```
Leu Val Phe Leu Ile His Ser Cys Ser Thr Met Glu Ser Gly Phe Phe
                 85                  90                  95

ctg gcc atg gct ttt gac cga tat gtg gcc att tgc aat cca tta aga   336
Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
            100                 105                 110

cat tca gct att ctg aca cgc gct gta att ggg aga gtg ggc cta gct   384
His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly Arg Val Gly Leu Ala
        115                 120                 125

att gtt ctc agg ggc ata gca ctt ctc agt cct cac tct ttc cta cta   432
Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro His Ser Phe Leu Leu
    130                 135                 140

cgc tgg ctt ccc tac tgc aga acc cat atc att tct cac acc tac tgt   480
Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys
145                 150                 155                 160

gag att gcc tgt gct gag aca aaa ttc cgc aga gcc tac agc ctc att   528
Glu Ile Ala Cys Ala Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile
                165                 170                 175

gtt gcc ttc ctt act ggg gtg gta gac ttt ata ttg atc att tat tct   576
Val Ala Phe Leu Thr Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser
            180                 185                 190

tat gtc ctc ata ctc cac act gtc ttc cag ctc cca tcc aaa gat gcc   624
Tyr Val Leu Ile Leu His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala
        195                 200                 205

cgg ctc aaa tct ttg ggc acc tgt ggc tcc cat gtc tgt gtc atc tta   672
Arg Leu Lys Ser Leu Gly Thr Cys Gly Ser His Val Cys Val Ile Leu
    210                 215                 220

gta tcc tat act cca gcc ttc ttc tcg ttt ctc acc cac agg ttt ggg   720
Val Ser Tyr Thr Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly
225                 230                 235                 240

cac cat gtg gct ccc cat ttt cac ata ttt gtg gcc aac atc tat ctt   768
His His Val Ala Pro His Phe His Ile Phe Val Ala Asn Ile Tyr Leu
                245                 250                 255

ctt gtc cca ccc atg gtg aac ccc att atc tat ggg gta aga acc aaa   816
Leu Val Pro Pro Met Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys
            260                 265                 270

agg att tgg gac agg ttc ctt aaa gtt ttc agg tta aat ttc cag tgc   864
Arg Ile Trp Asp Arg Phe Leu Lys Val Phe Arg Leu Asn Phe Gln Cys
        275                 280                 285

cac ata ttt gta atc act gat cat aaa aga ctc agt ata ata tct tct   912
His Ile Phe Val Ile Thr Asp His Lys Arg Leu Ser Ile Ile Ser Ser
    290                 295                 300

ttc ccc ata aaa gaa gca gcc tgc tgc aaa caa agg ttc tgc atg aag   960
Phe Pro Ile Lys Glu Ala Ala Cys Cys Lys Gln Arg Phe Cys Met Lys
305                 310                 315                 320

tta tgc agg cga                                                  972
Leu Cys Arg Arg
```

<210> 106
<211> 324
<212> PRT
<213> Homo sapiens

<400> 106
Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro Phe Cys Val Val Tyr
1 5 10 15
Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu Phe Ile Ile Lys Thr
20 25 30
Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe Leu Cys Met Leu Ala
35 40 45
Val Val Asp Leu Val Val Cys Ser Thr Ala Val Pro Lys Leu Leu Ser
50 55 60
Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe Glu Thr Cys Leu Ser
65 70 75 80
Leu Val Phe Leu Ile His Ser Cys Ser Thr Met Glu Ser Gly Phe Phe
85 90 95
Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
100 105 110
His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly Arg Val Gly Leu Ala
115 120 125
Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro His Ser Phe Leu Leu
130 135 140
Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys
145 150 155 160
Glu Ile Ala Cys Ala Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile
165 170 175
Val Ala Phe Leu Thr Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser
180 185 190
Tyr Val Leu Ile Leu His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala
195 200 205
Arg Leu Lys Ser Leu Gly Thr Cys Gly Ser His Val Cys Val Ile Leu
210 215 220
Val Ser Tyr Thr Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly
225 230 235 240
His His Val Ala Pro His Phe His Ile Phe Val Ala Asn Ile Tyr Leu
245 250 255
Leu Val Pro Pro Met Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys
260 265 270
Arg Ile Trp Asp Arg Phe Leu Lys Val Phe Arg Leu Asn Phe Gln Cys
275 280 285
His Ile Phe Val Ile Thr Asp His Lys Arg Leu Ser Ile Ile Ser Ser
290 295 300
Phe Pro Ile Lys Glu Ala Ala Cys Cys Lys Gln Arg Phe Cys Met Lys
305 310 315 320
Leu Cys Arg Arg

<210> 107
<211> 951
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(951)

<400> 107
aac cct gaa atg aat gtt gtc ctt tct gtg ctc ttt cta tta atc tat 48
Asn Pro Glu Met Asn Val Val Leu Ser Val Leu Phe Leu Leu Ile Tyr
1 5 10 15

```
ctc att act gtc ttg ggc aac ttt tgg att atc ata ata att ctg gct   96
Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile Ile Ile Ile Leu Ala
            20                  25                  30

agt gcc caa ctc cat tca ccc atg tac ttt ttc ctt agc cag ttg gct   144
Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu Ala
        35                  40                  45

ttc tta gat ttc tgc tat tct tca gtc ttg att cct aaa atg ttg gtg   192
Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile Pro Lys Met Leu Val
    50                  55                  60

aat tac ata gca gga cag aaa gtc atc tct tat cac ggt tgc ctc ctt   240
Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr His Gly Cys Leu Leu
65                  70                  75                  80

cag tat tcc ttt gtc agc ttg ttc ctg act act gaa tgc ttc ctc ctg   288
Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr Glu Cys Phe Leu Leu
                85                  90                  95

gct gcc atg gca tgt gat cgg tat ctc gct gtt tgc cac cca ctt cac   336
Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val Cys His Pro Leu His
            100                 105                 110

tac aaa gaa cat aga gtc cag gag cca att aga tgc tcg ctg ata tct   384
Tyr Lys Glu His Arg Val Gln Glu Pro Ile Arg Cys Ser Leu Ile Ser
        115                 120                 125

gtc tgg gtg ata agc agt ttg gcg ttc tgt gat tcc agc atc aat cat   432
Val Trp Val Ile Ser Ser Leu Ala Phe Cys Asp Ser Ser Ile Asn His
    130                 135                 140

ttt ttt tgt gac acc aca gct ctt tta gca ctc tcc tgt gta gat aca   480
Phe Phe Cys Asp Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Thr
145                 150                 155                 160

ttc ggc aca gaa atg gtg agc ttt gtc tta gct gga ttc act ctt ctt   528
Phe Gly Thr Glu Met Val Ser Phe Val Leu Ala Gly Phe Thr Leu Leu
                165                 170                 175

agc tct ctc ctt atc atc aca gtc act tat atc atc atc atc tca gcc   576
Ser Ser Leu Leu Ile Ile Thr Val Thr Tyr Ile Ile Ile Ile Ser Ala
            180                 185                 190

atc ctg agg atc cag tca gca gca ggc agg cag aag gcc ttc tcc acc   624
Ile Leu Arg Ile Gln Ser Ala Ala Gly Arg Gln Lys Ala Phe Ser Thr
        195                 200                 205

tgc gca tcc cac ctc atg gct gta act atc ttt tat ggg tct ctg att   672
Cys Ala Ser His Leu Met Ala Val Thr Ile Phe Tyr Gly Ser Leu Ile
    210                 215                 220

ttc acc tat ttg caa cct gat aac aca tca tcg ctg acc cag gcg cag   720
Phe Thr Tyr Leu Gln Pro Asp Asn Thr Ser Ser Leu Thr Gln Ala Gln
225                 230                 235                 240


gtg gca tct gta ttc tat acg att gtc att ccc atg ctg aat cca ctc   768
Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
                245                 250                 255
```

```
atc tac agt ctg agg aac aaa gat gtg aaa aat gct ctt ctg aga tgc   816
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Cys
            260                 265                 270

agt ggt gcc gtc tcg gct cac tgc aag ctc tgc ctc ctg aat tca cgc   864
Ser Gly Ala Val Ser Ala His Cys Lys Leu Cys Leu Leu Asn Ser Arg
        275                 280                 285

cat tct cct gcc tca gcc tcc caa gtc gct ggg act aca ggc gcc cgc   912
His Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Thr Gly Ala Arg
    290                 295                 300

cac cac gca agg cta ttt ttt tta ttt tta gta gag acg               951
His His Ala Arg Leu Phe Phe Leu Phe Leu Val Glu Thr
305                 310                 315
```

<210> 108
<211> 317
<212> PRT
<213> Homo sapiens

<400> 108

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Asn Pro Glu Met Asn Val Val Leu Ser Val Leu Phe Leu Leu Ile Tyr
 1               5                  10                  15
Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile Ile Ile Ile Leu Ala
            20                  25                  30
Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu Ala
        35                  40                  45
Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile Pro Lys Met Leu Val
    50                  55                  60
Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr His Gly Cys Leu Leu
65                  70                  75                  80
Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr Glu Cys Phe Leu Leu
                85                  90                  95
Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val Cys His Pro Leu His
            100                 105                 110
Tyr Lys Glu His Arg Val Gln Glu Pro Ile Arg Cys Ser Leu Ile Ser
        115                 120                 125
Val Trp Val Ile Ser Ser Leu Ala Phe Cys Asp Ser Ser Ile Asn His
    130                 135                 140
Phe Phe Cys Asp Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Thr
145                 150                 155                 160
Phe Gly Thr Glu Met Val Ser Phe Val Leu Ala Gly Phe Thr Leu Leu
                165                 170                 175
Ser Ser Leu Leu Ile Ile Thr Val Thr Tyr Ile Ile Ile Ile Ser Ala
            180                 185                 190
Ile Leu Arg Ile Gln Ser Ala Ala Gly Arg Gln Lys Ala Phe Ser Thr
        195                 200                 205
Cys Ala Ser His Leu Met Ala Val Thr Ile Phe Tyr Gly Ser Leu Ile
    210                 215                 220
Phe Thr Tyr Leu Gln Pro Asp Asn Thr Ser Ser Leu Thr Gln Ala Gln
225                 230                 235                 240
Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
                245                 250                 255
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Cys
            260                 265                 270

Ser Gly Ala Val Ser Ala His Cys Lys Leu Cys Leu Leu Asn Ser Arg
        275                 280                 285
His Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Thr Gly Ala Arg
    290                 295                 300
His His Ala Arg Leu Phe Phe Leu Phe Leu Val Glu Thr
```

305 310 315

<210> 109
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(948)

<400> 109

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caa tca aga att ggc ctt ttc gta ttc acc ctc att ttt ctc att ttc   48
Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu Ile Phe Leu Ile Phe
 1               5                  10                  15

cta atg gct cta att gga aat cta tcc atg att ctt ctc atc ttt ttg   96
Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu
            20                  25                  30

gac atc cat ctc cac aca cct atg tat ttc cta ctt agt cag ctc tcc   144
Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser
        35                  40                  45

ctc att gac cta aat tac atc tcc acc att gtt cca aag atg gtt tat   192
Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Val Tyr
    50                  55                  60

gat ttt ctg tat gga aac aag tct atc tcc ttc act gga tgt ggg att   240
Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile
65                  70                  75                  80

cag agt ttc ttc ttc ttg act tta gca gtt gca gaa ggg ctg ctc ctg   288
Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala Glu Gly Leu Leu Leu
                85                  90                  95

aca tca atg gcc tat gat cgt tat gtg gcc att tgc ttt cct ctc cac   336
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
            100                 105                 110

tat ccc atc cgt ata agc aaa aga gtg tgt gtg atg atg ata aca gga   384
Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val Met Met Ile Thr Gly
        115                 120                 125

tct tgg atg ata agc tct atc aac tct tgt gct cac aca gta tat gca   432
Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala His Thr Val Tyr Ala
    130                 135                 140

ctc tgt atc cca tat tgc aag tcc aga gcc atc aat cat ttt ttc tcc   480
Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe Phe Ser
145                 150                 155                 160

tgc aca gac act tgg gtc tat gag agc aca gtg ttt ttg agc agc acc   528
Cys Thr Asp Thr Trp Val Tyr Glu Ser Thr Val Phe Leu Ser Ser Thr
                165                 170                 175

atc ttt ctt gtg ctt cct ttc act ggt att gca tgt tcc tat ggc cgg   576
Ile Phe Leu Val Leu Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Arg
            180                 185                 190

gtt ctc ctt gct gtc tac cgc atg cac tct gca aaa ggg agg aat aag   624
Val Leu Leu Ala Val Tyr Arg Met His Ser Ala Lys Gly Arg Asn Lys
```

```
        195                 200                 205

gtc tat tca acc tgt agc acc cac ctc act gtg gtg tac ttc tac tat   672
Val Tyr Ser Thr Cys Ser Thr His Leu Thr Val Val Tyr Phe Tyr Tyr
    210                 215                 220

gca ccc ttt gct tat acc tat gta cgt gca aga tcc ctg cga tct cca   720
Ala Pro Phe Ala Tyr Thr Tyr Val Arg Ala Arg Ser Leu Arg Ser Pro
225                 230                 235                 240

acc gag gac aag att ctg gct gtt ttc tac acc atc ctc acc cca atg   768
Thr Glu Asp Lys Ile Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met
                245                 250                 255

ctc aac ccc atc atc tac agc ctg aga aac aag gag agc ttc tgc aca   816
Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ser Phe Cys Thr
            260                 265                 270

gca aaa gaa act acc atc aga gtg aac agg caa cct aca gaa tgg gag   864
Ala Lys Glu Thr Thr Ile Arg Val Asn Arg Gln Pro Thr Glu Trp Glu
        275                 280                 285

aaa att ttt gca acc tac tca tct gac aaa ggg cta ata tcc aga atc   912
Lys Ile Phe Ala Thr Tyr Ser Ser Asp Lys Gly Leu Ile Ser Arg Ile
    290                 295                 300

tac aat gaa ctc aaa caa act tac aag aaa aaa aca                   948
Tyr Asn Glu Leu Lys Gln Thr Tyr Lys Lys Lys Thr
305                 310                 315
```

<210> 110
<211> 316
<212> PRT
<213> Homo sapiens

<400> 110

```
Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu Ile Phe Leu Ile Phe
 1               5                  10                  15
Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu
            20                  25                  30
Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser
        35                  40                  45
Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Val Tyr
    50                  55                  60
Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile
65                  70                  75                  80
Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala Glu Gly Leu Leu Leu
                85                  90                  95
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
            100                 105                 110
Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val Met Met Ile Thr Gly
        115                 120                 125
Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala His Thr Val Tyr Ala
    130                 135                 140

Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe Phe Ser
145                 150                 155                 160
Cys Thr Asp Thr Trp Val Tyr Glu Ser Thr Val Phe Leu Ser Ser Thr
                165                 170                 175
Ile Phe Leu Val Leu Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Arg
            180                 185                 190
Val Leu Leu Ala Val Tyr Arg Met His Ser Ala Lys Gly Arg Asn Lys
```

```
        195                 200                 205
Val Tyr Ser Thr Cys Ser Thr His Leu Thr Val Val Tyr Phe Tyr Tyr
    210                 215                 220
Ala Pro Phe Ala Tyr Thr Tyr Val Arg Ala Arg Ser Leu Arg Ser Pro
225                 230                 235                 240
Thr Glu Asp Lys Ile Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met
                245                 250                 255
Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ser Phe Cys Thr
            260                 265                 270
Ala Lys Glu Thr Thr Ile Arg Val Asn Arg Gln Pro Thr Glu Trp Glu
        275                 280                 285
Lys Ile Phe Ala Thr Tyr Ser Ser Asp Lys Gly Leu Ile Ser Arg Ile
    290                 295                 300
Tyr Asn Glu Leu Lys Gln Thr Tyr Lys Lys Lys Thr
305                 310                 315


<210> 111
<211> 939
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(939)

<400> 111
cca tca aga att gac ctt ttc ttc ttc att ctc att gtt ttc att ttc   48
Pro Ser Arg Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe Ile Phe
 1               5                  10                  15

ctg atg gct cta att gga aac ctg tcc atg att ctt ctc atc ttc ttg   96
Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu
            20                  25                  30

gac acc cat ctc cac aca ccc atg tat ttc cta ctg agt cag ctc tcc   144
Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser
        35                  40                  45

ctc att gac cta aat tac atc tcc acc att gtt cct aag atg gca tct   192
Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser
    50                  55                  60

gat ttt ctg cat gga aac aag tct atc tcc ttc act ggg tgt ggg att   240
Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile
65                  70                  75                  80

cag agt ttc ttc ttc ttg gca tta gga ggt gca gaa gca cta ctt ttg   288
Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu
                85                  90                  95

gca tct atg gcc tat gat cgt tac att gct att tgc ttt cct ctc cac   336
Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His
            100                 105                 110

tat ctc atc cgc atg agc aaa aga gtg tgt gtg ctg atg ata aca ggg   384
Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile Thr Gly
        115                 120                 125

tct tgg atc ata ggc tcg atc aat gct tgt gct cac act gta tat gta   432
Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr Val
    130                 135                 140
```

```
ctc cat att cct tat tgc cga tcc agg gcc atc aat cat ttc ttc tgt   480
Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe Phe Cys
145                 150                 155                 160

gat gtc cca gca atg ggc aca gtg ttt ttg agt gcc acc atc ttt ctc   528
Asp Val Pro Ala Met Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu
                165                 170                 175

gtg ttt ccc ttc att ggt att tca tgt tcc tat ggc cag gtt ctc ttt   576
Val Phe Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe
            180                 185                 190

gct gtc tac cac atg aaa tct gca gaa ggg agg aag aaa gcc tat ttg   624
Ala Val Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu
        195                 200                 205

acc tgc agc acc cac ctc act gta gta act ttc tac tat gca cct ttt   672
Thr Cys Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe
    210                 215                 220

gtc tac act tat cta cgt cca aga tcc ctg cga tct cca aca gag gac   720
Val Tyr Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp
225                 230                 235                 240

aag gtt ctg gct gtc ttc tac acc atc ctc acc cca atg ctc aac ccc   768
Lys Val Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
                245                 250                 255

atc atc tat agc ctg agg aac aag gag agc aag aga aag aaa aga aag   816
Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ser Lys Arg Lys Lys Arg Lys
            260                 265                 270

gaa aga aag aga aaa aga aag aaa aga aag aaa gaa aga gaa aga aag   864
Glu Arg Lys Arg Lys Arg Lys Lys Arg Lys Lys Glu Arg Glu Arg Lys
        275                 280                 285

aga gaa aga gag aaa gag aaa gaa aga aaa gaa agg aaa gaa aga gaa   912
Arg Glu Arg Glu Lys Glu Lys Glu Arg Lys Glu Arg Lys Glu Arg Glu
    290                 295                 300

aaa gaa aga aaa gaa aga aag aaa gag                             939
Lys Glu Arg Lys Glu Arg Lys Lys Glu
305                 310
```

<210> 112
<211> 313
<212> PRT
<213> Homo sapiens

<400> 112

```
Pro Ser Arg Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe Ile Phe
 1               5                  10                  15

Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu
            20                  25                  30
Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser
        35                  40                  45
Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser
    50                  55                  60
Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile
65                  70                  75                  80
Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu
```

```
                85                  90                  95
Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His
            100                 105                 110
Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile Thr Gly
        115                 120                 125
Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr Val
    130                 135                 140
Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe Phe Cys
145                 150                 155                 160
Asp Val Pro Ala Met Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu
                165                 170                 175
Val Phe Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe
            180                 185                 190
Ala Val Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu
        195                 200                 205
Thr Cys Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe
    210                 215                 220
Val Tyr Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp
225                 230                 235                 240
Lys Val Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
                245                 250                 255
Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ser Lys Arg Lys Lys Arg Lys
            260                 265                 270
Glu Arg Lys Arg Lys Arg Lys Lys Arg Lys Lys Glu Arg Glu Arg Lys
        275                 280                 285
Arg Glu Arg Glu Lys Glu Lys Glu Arg Lys Glu Arg Lys Glu Arg Glu
    290                 295                 300
Lys Glu Arg Lys Glu Arg Lys Lys Glu
305                 310
```

<210> 113
<211> 966
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(966)

<400> 113

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tcc cga gaa ctg agc cag gtc tta ttt acc ttc ctg ttt ttg gtg tac   48
Ser Arg Glu Leu Ser Gln Val Leu Phe Thr Phe Leu Phe Leu Val Tyr
 1               5                  10                  15

atg aca act cta atg gga aac ttc ctc atc atg gtt aca gtt acc tgt   96
Met Thr Thr Leu Met Gly Asn Phe Leu Ile Met Val Thr Val Thr Cys
            20                  25                  30

gaa tct cac ctt cat acg ccc atg tac ttc ctg ctc cgc aac ctg tct  144
Glu Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Arg Asn Leu Ser
        35                  40                  45

att ctt gac atc tgc ttt tcc tcc atc aca gct cct aag gtc ctg ata  192
Ile Leu Asp Ile Cys Phe Ser Ser Ile Thr Ala Pro Lys Val Leu Ile
    50                  55                  60

gat ctt cta tca gag aca aaa acc atc tcc ttc agt ggc tgt gtc act  240
Asp Leu Leu Ser Glu Thr Lys Thr Ile Ser Phe Ser Gly Cys Val Thr
65                  70                  75                  80

caa atg ttc ttc ttc cac ctt ctg ggg gga gca gac gtt ttt tct ctc  288
Gln Met Phe Phe Phe His Leu Leu Gly Gly Ala Asp Val Phe Ser Leu
```

```
                85                  90                  95

tct gtg atg gcg ttt gac cgc tat ata gcc atc tcc aag ccc ctg cac   336
Ser Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Ser Lys Pro Leu His
            100                 105                 110

tat atg acc atc atg agt agg ggg cga tgc aca ggc ctc atc gtg ggc   384
Tyr Met Thr Ile Met Ser Arg Gly Arg Cys Thr Gly Leu Ile Val Gly
        115                 120                 125

ttc ctg ggt ggg ggg ctt gtc cac tcc ata gcg cag att tct cta ttg   432
Phe Leu Gly Gly Gly Leu Val His Ser Ile Ala Gln Ile Ser Leu Leu
    130                 135                 140

ctc cca ctc cct gtc tgt gga ccc aat gtt ctt gac act ttc tac tgc   480
Leu Pro Leu Pro Val Cys Gly Pro Asn Val Leu Asp Thr Phe Tyr Cys
145                 150                 155                 160

gat gtc ccc cag gtc ctc aaa ctt gcc tgc act gac acc ttc act ctg   528
Asp Val Pro Gln Val Leu Lys Leu Ala Cys Thr Asp Thr Phe Thr Leu
                165                 170                 175

gag ctc ctg atg att tca aat aat ggg tta gtc agt tgg ttt gta ttc   576
Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Val Ser Trp Phe Val Phe
            180                 185                 190

ttc ttt ctc ctc ata tct tac acg gtc atc ttg atg atg ctg agg tct   624
Phe Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met Leu Arg Ser
        195                 200                 205

cac act ggg gaa ggc agg agg aaa gcc atc tcc acc tgc acc tcc cac   672
His Thr Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys Thr Ser His
    210                 215                 220

atc acc gtg gtg acc ctg cat ttc gtg ccc tgc atc tat gtc tat gcc   720
Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val Tyr Ala
225                 230                 235                 240

cgg ccc ttc act gcc ctc ccc aca gac act gcc atc tct gtc acc ttc   768
Arg Pro Phe Thr Ala Leu Pro Thr Asp Thr Ala Ile Ser Val Thr Phe
                245                 250                 255

act gtc atc tcc cct ttg ctc aat cct ata att tac acg ctg agg aat   816
Thr Val Ile Ser Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn
            260                 265                 270

cag gaa atg aac aac aga tca aga cac ttg tca aaa aaa aaa aag aaa   864
Gln Glu Met Asn Asn Arg Ser Arg His Leu Ser Lys Lys Lys Lys Lys
        275                 280                 285


aga aaa gac aaa aag aaa cca gca tgc gca aag aaa gaa aat gag gtg   912
Arg Lys Asp Lys Lys Lys Pro Ala Cys Ala Lys Lys Glu Asn Glu Val
    290                 295                 300

aga ttg tgc cac att tgt gta aca gtg aac tca gtg cag cca tgg cgt   960
Arg Leu Cys His Ile Cys Val Thr Val Asn Ser Val Gln Pro Trp Arg
305                 310                 315                 320

aat aca                                                          966
Asn Thr
```

<210> 114
<211> 322
<212> PRT
<213> Homo sapiens

<400> 114
Ser Arg Glu Leu Ser Gln Val Leu Phe Thr Phe Leu Phe Leu Val Tyr
1 5 10 15
Met Thr Thr Leu Met Gly Asn Phe Leu Ile Met Val Thr Val Thr Cys
20 25 30
Glu Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Arg Asn Leu Ser
35 40 45
Ile Leu Asp Ile Cys Phe Ser Ser Ile Thr Ala Pro Lys Val Leu Ile
50 55 60
Asp Leu Leu Ser Glu Thr Lys Thr Ile Ser Phe Ser Gly Cys Val Thr
65 70 75 80
Gln Met Phe Phe Phe His Leu Leu Gly Gly Ala Asp Val Phe Ser Leu
85 90 95
Ser Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Ser Lys Pro Leu His
100 105 110
Tyr Met Thr Ile Met Ser Arg Gly Arg Cys Thr Gly Leu Ile Val Gly
115 120 125
Phe Leu Gly Gly Gly Leu Val His Ser Ile Ala Gln Ile Ser Leu Leu
130 135 140
Leu Pro Leu Pro Val Cys Gly Pro Asn Val Leu Asp Thr Phe Tyr Cys
145 150 155 160
Asp Val Pro Gln Val Leu Lys Leu Ala Cys Thr Asp Thr Phe Thr Leu
165 170 175
Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Val Ser Trp Phe Val Phe
180 185 190
Phe Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met Leu Arg Ser
195 200 205
His Thr Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys Thr Ser His
210 215 220
Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val Tyr Ala
225 230 235 240
Arg Pro Phe Thr Ala Leu Pro Thr Asp Thr Ala Ile Ser Val Thr Phe
245 250 255
Thr Val Ile Ser Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn
260 265 270
Gln Glu Met Asn Asn Arg Ser Arg His Leu Ser Lys Lys Lys Lys Lys
275 280 285
Arg Lys Asp Lys Lys Lys Pro Ala Cys Ala Lys Lys Glu Asn Glu Val
290 295 300
Arg Leu Cys His Ile Cys Val Thr Val Asn Ser Val Gln Pro Trp Arg
305 310 315 320
Asn Thr

<210> 115
<211> 975
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(975)

<400> 115
tgg caa caa cag cag gtg cta ctc ttt gca ctt ttc ctg tgt ctc tat 48

```
Trp Gln Gln Gln Gln Val Leu Leu Phe Ala Leu Phe Leu Cys Leu Tyr
 1               5                  10                  15

tta aca ggg ctg ttt gga aac tta ctc atc ttg ctg gcc att ggc tcg   96
Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala Ile Gly Ser
            20                  25                  30

gat cac tgc ctt cac aca ccc atg tat ttc ttc ctt gcc aat ctg tcc   144
Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser
        35                  40                  45

ttg gta gac ctc tgc ctt ccc tca gcc aca gtc ccc aag atg cta ctg   192
Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys Met Leu Leu
    50                  55                  60

aac atc caa acc caa acc caa acc atc tcc tat ccc ggc tgc ctg gct   240
Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly Cys Leu Ala
65                  70                  75                  80

cag atg tat ttc tgt atg atg ttt gcc aat atg gac aat ttt ctt ctc   288
Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn Phe Leu Leu
                85                  90                  95

aca gtg atg gca tat gac cgt tac gtg gcc atc tgt cac cct tta cat   336
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
            100                 105                 110

tac tcc acc att atg gcc ctg cgc ctc tgt gcc tct ctg gta gct gca   384
Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu Val Ala Ala
        115                 120                 125

cct tgg gtc att gcc att ttg aac cct ctc ttg cac act ctt atg atg   432
Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr Leu Met Met
    130                 135                 140

gcc cat ctg cac ttc tgc tct gat aat gtt atc cac cat ttc ttc tgt   480
Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His Phe Phe Cys
145                 150                 155                 160

gat atc aac tct ctc ctc cct ctg tcc tgt tcc gac acc agt ctt aat   528
Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr Ser Leu Asn
                165                 170                 175

cag ttg agt gtt ctg gct acg gtg ggg ctg atc ttt gtg gta cct tca   576
Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val Val Pro Ser
            180                 185                 190

gtg tgt atc ctg gta tcc tat atc ctc att gtt tct gct gtg atg aaa   624
Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala Val Met Lys
        195                 200                 205

gtc cct tct gcc caa gga aaa ctc aag gct ttc tct acc tgt gga tct   672
Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr Cys Gly Ser
    210                 215                 220

cac ctt gcc ttg gtc att ctt ttc tat gga gca atc aca ggg gtc tat   720
His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr Gly Val Tyr
225                 230                 235                 240

atg agc ccc tta tcc aat cac tct act gaa aaa gac tca gcc gca tca   768
Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser Ala Ala Ser
                245                 250                 255
```

```
gtc att ttt atg gtt gta gca cct gtg ttg aat cca ttc att tac agt   816
Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe Ile Tyr Ser
            260                 265                 270

tta aga aac aat gaa ctg aag ggg act tta aaa aag acc cta agc cga   864
Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr Leu Ser Arg
        275                 280                 285

ccg ggc gcg gtg gct cac gcc tgt aat ccc agc act ttg gga ggc cga   912
Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr Leu Gly Gly Arg
    290                 295                 300

ggc gga aat aca tgg aca gaa gca aaa tat gtt cat aga gaa gta cat   960
Gly Gly Asn Thr Trp Thr Glu Ala Lys Tyr Val His Arg Glu Val His
305                 310                 315                 320

ata atg atc aag aga                                              975
Ile Met Ile Lys Arg
                325
```

<210> 116
<211> 325
<212> PRT
<213> Homo sapiens

<400> 116

```
Trp Gln Gln Gln Gln Val Leu Leu Phe Ala Leu Phe Leu Cys Leu Tyr
 1               5                  10                  15
Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala Ile Gly Ser
            20                  25                  30
Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser
        35                  40                  45
Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys Met Leu Leu
    50                  55                  60
Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly Cys Leu Ala
65                  70                  75                  80
Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn Phe Leu Leu
                85                  90                  95
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
            100                 105                 110
Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu Val Ala Ala
        115                 120                 125
Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr Leu Met Met
    130                 135                 140
Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His Phe Phe Cys
145                 150                 155                 160
Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr Ser Leu Asn
                165                 170                 175

Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val Val Pro Ser
            180                 185                 190
Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala Val Met Lys
        195                 200                 205
Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr Cys Gly Ser
    210                 215                 220
His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr Gly Val Tyr
225                 230                 235                 240
Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser Ala Ala Ser
                245                 250                 255
Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe Ile Tyr Ser
            260                 265                 270
Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr Leu Ser Arg
```

```
        275                 280                 285
Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr Leu Gly Gly Arg
    290                 295                 300
Gly Gly Asn Thr Trp Thr Glu Ala Lys Tyr Val His Arg Glu Val His
305                 310                 315                 320
Ile Met Ile Lys Arg
                325
```

<210> 117
<211> 963
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(963)

<400> 117

```
tac cca gaa atc cag gtt cca ctc ttt ctg gtt ttc ttg ttc gtc tac   48
Tyr Pro Glu Ile Gln Val Pro Leu Phe Leu Val Phe Leu Phe Val Tyr
 1               5                  10                  15

aca gtc act gta gtg ggg aac ttg ggc atg ata ata atc atc aga ctc   96
Thr Val Thr Val Val Gly Asn Leu Gly Met Ile Ile Ile Ile Arg Leu
            20                  25                  30

aat tca aaa ctc cat aca atc atg tgc ttt ttc ctt agt cac ttg tcc   144
Asn Ser Lys Leu His Thr Ile Met Cys Phe Phe Leu Ser His Leu Ser
        35                  40                  45

ttg aca gac ttc tgt ttt tcc act gta gtt aca cct aaa ctg ttg gag   192
Leu Thr Asp Phe Cys Phe Ser Thr Val Val Thr Pro Lys Leu Leu Glu
    50                  55                  60

aac ttg gtt gtg gaa tac aga acc atc tct ttc tct ggt tgc atc atg   240
Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Ser Gly Cys Ile Met
65                  70                  75                  80

caa ttt tgt ttt gct tgc att ttt gga gtg aca gaa act ttc atg tta   288
Gln Phe Cys Phe Ala Cys Ile Phe Gly Val Thr Glu Thr Phe Met Leu
                85                  90                  95

gca gcg atg gct tat gac cgt ttt gtg gca gtt tgt aaa ccc ttg ctg   336
Ala Ala Met Ala Tyr Asp Arg Phe Val Ala Val Cys Lys Pro Leu Leu
            100                 105                 110



tat acc act att atg tct cag aag ctc tgt gct ctt ctg gtg gct ggg   384
Tyr Thr Thr Ile Met Ser Gln Lys Leu Cys Ala Leu Leu Val Ala Gly
        115                 120                 125

tcc tat aca tgg ggg ata gtg tgc tcc ctg ata ctc aca tat ttt ctt   432
Ser Tyr Thr Trp Gly Ile Val Cys Ser Leu Ile Leu Thr Tyr Phe Leu
    130                 135                 140

ctt gac tta tcg ttt tgt gaa tct acc ttc ata aat aat ttt atc tct   480
Leu Asp Leu Ser Phe Cys Glu Ser Thr Phe Ile Asn Asn Phe Ile Ser
145                 150                 155                 160

ttc aac tcc acc tta tac tat aaa ata tac cac caa acc ttc tcc tgt   528
Phe Asn Ser Thr Leu Tyr Tyr Lys Ile Tyr His Gln Thr Phe Ser Cys
```

```
                165                 170                 175

ata tgt gag cac ttt ctg cca atg tgt aca cta ctg atc atc ctc act   576
Ile Cys Glu His Phe Leu Pro Met Cys Thr Leu Leu Ile Ile Leu Thr
            180                 185                 190

tcc tat gtt ttc att ttt gtg act gta cta aaa atc cgt tct gtt agt   624
Ser Tyr Val Phe Ile Phe Val Thr Val Leu Lys Ile Arg Ser Val Ser
        195                 200                 205

ggg cgc cac aaa gcc ttc tcc acc tgg gcc tcc cac ctg act tct atc   672
Gly Arg His Lys Ala Phe Ser Thr Trp Ala Ser His Leu Thr Ser Ile
    210                 215                 220

acc atc ttc cat ggg acc atc ctt ttc ctt tac tgt gta ccc aac tcc   720
Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser
225                 230                 235                 240

aaa aac tct cgg caa aca gtc aaa gtg gcc tct gta ttt tac aca gtt   768
Lys Asn Ser Arg Gln Thr Val Lys Val Ala Ser Val Phe Tyr Thr Val
                245                 250                 255

gtc aac ccc atg ctg aac cct ctg atc tac agc cta agg aat aaa gac   816
Val Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp
            260                 265                 270

gtg aag gat gct ttc tgg aag tta ata cat aca caa tca aga agg agg   864
Val Lys Asp Ala Phe Trp Lys Leu Ile His Thr Gln Ser Arg Arg Arg
        275                 280                 285

cag agc ttg agg agg tcc ttg aga aat tcc cat tta atg acc acc agc   912
Gln Ser Leu Arg Arg Ser Leu Arg Asn Ser His Leu Met Thr Thr Ser
    290                 295                 300

att gaa gaa gga gtc acc cac acc agt acc att ctg gag ctc tgc tca   960
Ile Glu Glu Gly Val Thr His Thr Ser Thr Ile Leu Glu Leu Cys Ser
305                 310                 315                 320

tcc                                                               963
Ser
```

<210> 118
<211> 321
<212> PRT
<213> Homo sapiens

<400> 118

```
Tyr Pro Glu Ile Gln Val Pro Leu Phe Leu Val Phe Leu Phe Val Tyr
 1               5                  10                  15
Thr Val Thr Val Val Gly Asn Leu Gly Met Ile Ile Ile Ile Arg Leu
            20                  25                  30
Asn Ser Lys Leu His Thr Ile Met Cys Phe Phe Leu Ser His Leu Ser
        35                  40                  45
Leu Thr Asp Phe Cys Phe Ser Thr Val Val Thr Pro Lys Leu Leu Glu
    50                  55                  60
Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Ser Gly Cys Ile Met
65                  70                  75                  80
Gln Phe Cys Phe Ala Cys Ile Phe Gly Val Thr Glu Thr Phe Met Leu
                85                  90                  95
Ala Ala Met Ala Tyr Asp Arg Phe Val Ala Val Cys Lys Pro Leu Leu
            100                 105                 110
```

```
Tyr Thr Thr Ile Met Ser Gln Lys Leu Cys Ala Leu Leu Val Ala Gly
        115                 120                 125
Ser Tyr Thr Trp Gly Ile Val Cys Ser Leu Ile Leu Thr Tyr Phe Leu
    130                 135                 140
Leu Asp Leu Ser Phe Cys Glu Ser Thr Phe Ile Asn Asn Phe Ile Ser
145                 150                 155                 160
Phe Asn Ser Thr Leu Tyr Tyr Lys Ile Tyr His Gln Thr Phe Ser Cys
                165                 170                 175
Ile Cys Glu His Phe Leu Pro Met Cys Thr Leu Leu Ile Ile Leu Thr
            180                 185                 190
Ser Tyr Val Phe Ile Phe Val Thr Val Leu Lys Ile Arg Ser Val Ser
        195                 200                 205
Gly Arg His Lys Ala Phe Ser Thr Trp Ala Ser His Leu Thr Ser Ile
    210                 215                 220
Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser
225                 230                 235                 240
Lys Asn Ser Arg Gln Thr Val Lys Val Ala Ser Val Phe Tyr Thr Val
                245                 250                 255
Val Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp
            260                 265                 270
Val Lys Asp Ala Phe Trp Lys Leu Ile His Thr Gln Ser Arg Arg Arg
        275                 280                 285
Gln Ser Leu Arg Arg Ser Leu Arg Asn Ser His Leu Met Thr Thr Ser
    290                 295                 300
Ile Glu Glu Gly Val Thr His Thr Ser Thr Ile Leu Glu Leu Cys Ser
305                 310                 315                 320
Ser
```

<210> 119
<211> 927
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(927)

<400> 119

```
cca ctc agg cta agg aca ctc ttt ttt gtg ttc ttt ttt cta atc tac   48
Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe Leu Ile Tyr
 1               5                  10                  15

atc ctg act cag ctg gga aac ctg ctt att tta atc act gtc tgg gca   96
Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr Val Trp Ala
            20                  25                  30

gac cca agg ctc cat gcc cgc ccc atg tac atc ttt ctt ggt gtt ctc   144
Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu Gly Val Leu
        35                  40                  45

tca gtc att gat atg agc atc tcc tcc atc att gtc cct cgc ctc atg   192
Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro Arg Leu Met
    50                  55                  60

atg aac ttc act tta ggt gtc aaa ccc atc cca ttt ggt ggc tgt gtt   240
Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly Gly Cys Val
65                  70                  75                  80

gct caa ctc tat ttc tat cac ttc ctg ggc agc acc cag tgc ttc ctc   288
Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln Cys Phe Leu
                85                  90                  95
```

```
tac acc cta atg gcc tat gac agg tac ctg gca ata tgt cag ccc ctg   336
Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu
            100                 105                 110

cgc tac cct gtg ctc atg act gct aag ctg agc gcc ttg ctt gtg gct   384
Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu Leu Val Ala
        115                 120                 125

gga gcc tgg atg gca gga tcc atc cat ggg gct ctc cag gcc atc cta   432
Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln Ala Ile Leu
    130                 135                 140

acc ttc cgc ctg ccc tac tgt ggg ccc aat cag gtg gat tac ttc ttc   480
Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe
145                 150                 155                 160

ttc aac gag ctg gtg acg ttt gta gac att ggg gtg gtg gtt gcc agt   528
Phe Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val Ala Ser
                165                 170                 175

tgc ttc tcc ctg atc ctc ctc tcc tac ata cag atc att cag gcc atc   576
Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln Ala Ile
            180                 185                 190

ctg aga atc cac aca gct gat ggg cgg cgc cgg gct ttt tca act tgt   624
Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser Thr Cys
        195                 200                 205

gga gcc cat gta acc gtg gtc acc gtg tac tat gtg ccc tgt gcc ttc   672
Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys Ala Phe
    210                 215                 220

atc tac ctg agg cct gaa acc aac agc ccc ctg gat ggg gca gct gcc   720
Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala Ala Ala
225                 230                 235                 240

cta gtc ccc acg gcc atc act cct ttc ctc aac ccc ctt atc tac act   768
Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
                245                 250                 255

ctg cgg aac caa gag gtg aag ctg gcc ctg aaa aga atg ctc aga agc   816
Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu Arg Ser
            260                 265                 270

cca aga act ccg agt gag cac ttt ggg agg cca agg cgg gtg gat cac   864
Pro Arg Thr Pro Ser Glu His Phe Gly Arg Pro Arg Arg Val Asp His
        275                 280                 285

ctg agg tcg gga gtt cga gac cag cct aac caa cat gga gaa act gca   912
Leu Arg Ser Gly Val Arg Asp Gln Pro Asn Gln His Gly Glu Thr Ala
    290                 295                 300

tct tta cca aaa ata                                             927
Ser Leu Pro Lys Ile
305
```

<210> 120
<211> 309
<212> PRT
<213> Homo sapiens

<400> 120
Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe Leu Ile Tyr
1 5 10 15
Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr Val Trp Ala
20 25 30
Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu Gly Val Leu
35 40 45
Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro Arg Leu Met
50 55 60
Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly Gly Cys Val
65 70 75 80
Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln Cys Phe Leu
85 90 95
Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu
100 105 110
Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu Leu Val Ala
115 120 125
Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln Ala Ile Leu
130 135 140
Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe
145 150 155 160
Phe Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val Ala Ser
165 170 175
Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln Ala Ile
180 185 190
Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser Thr Cys
195 200 205
Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys Ala Phe
210 215 220
Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala Ala Ala
225 230 235 240
Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
245 250 255
Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu Arg Ser
260 265 270
Pro Arg Thr Pro Ser Glu His Phe Gly Arg Pro Arg Arg Val Asp His
275 280 285
Leu Arg Ser Gly Val Arg Asp Gln Pro Asn Gln His Gly Glu Thr Ala
290 295 300
Ser Leu Pro Lys Ile
305

<210> 121
<211> 972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(972)

<400> 121
gat cct ata gtg aca ccc cac tta atc agc ctc tac ttc ata gtg ctt 48
Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu
1 5 10 15

att ggc ggg ctg gtg ggt gtc att tcc att ctt ttc ctc ctg gtg aaa 96
Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys
20 25 30

atg aac acc cgg tca gtg acc acc atg gcg gtc att aac ttg gtg gtg 144
Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val

```
        35                  40                  45

gtc cac agc gtt ttt ctg ctg aca gtg cca ttt cgc ttg acc tac ctc   192
Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu
     50                  55                  60

atc aag aag act tgg atg ttt ggg ctg ccc ttc tgc aaa ttt gtg agt   240
Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser
 65                  70                  75                  80

gcc atg ctg cac atc cac atg tac ctc acg ttc cta ttc tat gtg gtg   288
Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val
                 85                  90                  95

atc ctg gtc acc aga tac ctc atc ttc ttc aag tgc aaa gac aaa gtg   336
Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val
            100                 105                 110

gaa ttc tac aga aaa ctg cat gct gtg gct gcc agt gct ggc atg tgg   384
Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp
        115                 120                 125

acg ctg gtg att gtc att gtg gta ccc ctg gtt gtc tcc cgg tat gga   432
Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly
    130                 135                 140

atc cat gag gaa tac aat gag gag cac tgt ttt aaa ttt cac aaa gag   480
Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu
145                 150                 155                 160

ctt gct tac aca tat gtg aaa atc atc aac tat atg ata gtc att ttt   528
Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe
                165                 170                 175

gtc ata gcc gtt gct gtg att ctg ttg gtc ttc cag gtc ttc atc att   576
Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile
            180                 185                 190

atg ttg atg gtg cag aag cta cgc cac tct tta cta tcc cac cag gag   624
Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu
        195                 200                 205

ttc tgg gct cag ctg aaa aac cta ttt ttt ata ggg gtc atc ctt gtt   672
Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val
    210                 215                 220

tgt ttc ctt ccc tac cag ccc cat tgt gtg atg ttc ccc tcc ctg tgt   720
Cys Phe Leu Pro Tyr Gln Pro His Cys Val Met Phe Pro Ser Leu Cys
225                 230                 235                 240

cca tgt gtt ttc att gtt caa ctc cca ctt cta agt gag aac atg cgg   768
Pro Cys Val Phe Ile Val Gln Leu Pro Leu Leu Ser Glu Asn Met Arg
                245                 250                 255

tgt ttg gtt ttc tgt tcc tgt ttg att cat ttt tta ttg tat ata ttt   816
Cys Leu Val Phe Cys Ser Cys Leu Ile His Phe Leu Leu Tyr Ile Phe
            260                 265                 270

ata gtg cac aac atg agg tat tca tac atg tat aac ttc gtc agc tgt   864
Ile Val His Asn Met Arg Tyr Ser Tyr Met Tyr Asn Phe Val Ser Cys
        275                 280                 285
```

```
cct ttg cca gca tgt aat gca gtg atg caa tgc tct ggt agt aat ttg   912
Pro Leu Pro Ala Cys Asn Ala Val Met Gln Cys Ser Gly Ser Asn Leu
    290                 295                 300

gaa caa tcc agg aag caa tat tct cag tgt tca agg ccc ggc act gcc   960
Glu Gln Ser Arg Lys Gln Tyr Ser Gln Cys Ser Arg Pro Gly Thr Ala
305                 310                 315                 320

cgg ggg aaa tta                                                  972
Arg Gly Lys Leu
```

<210> 122
<211> 324
<212> PRT
<213> Homo sapiens

<400> 122

```
Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu
 1               5                  10                  15
Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys
            20                  25                  30
Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val
        35                  40                  45
Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu
    50                  55                  60
Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser
65                  70                  75                  80
Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val
                85                  90                  95
Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val
            100                 105                 110
Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp
        115                 120                 125
Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly
    130                 135                 140
Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu
145                 150                 155                 160
Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe
                165                 170                 175

Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile
            180                 185                 190
Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu
        195                 200                 205
Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val
    210                 215                 220
Cys Phe Leu Pro Tyr Gln Pro His Cys Val Met Phe Pro Ser Leu Cys
225                 230                 235                 240
Pro Cys Val Phe Ile Val Gln Leu Pro Leu Leu Ser Glu Asn Met Arg
                245                 250                 255
Cys Leu Val Phe Cys Ser Cys Leu Ile His Phe Leu Leu Tyr Ile Phe
            260                 265                 270
Ile Val His Asn Met Arg Tyr Ser Tyr Met Tyr Asn Phe Val Ser Cys
        275                 280                 285
Pro Leu Pro Ala Cys Asn Ala Val Met Gln Cys Ser Gly Ser Asn Leu
    290                 295                 300
Glu Gln Ser Arg Lys Gln Tyr Ser Gln Cys Ser Arg Pro Gly Thr Ala
305                 310                 315                 320
Arg Gly Lys Leu
```

<210> 123
<211> 933
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(933)

<400> 123

```
cat gtt ctt aat ttc caa gaa ctc ttt ttt ctt gtc ttc gga gtt tca   48
His Val Leu Asn Phe Gln Glu Leu Phe Phe Leu Val Phe Gly Val Ser
 1               5                  10                  15

aca ctt att gtt gtt ttt tta atg gtg ctc ata att ctg acc aca ctc   96
Thr Leu Ile Val Val Phe Leu Met Val Leu Ile Ile Leu Thr Thr Leu
            20                  25                  30

gtt ggc aat ctg ata gtt att gtt tct ata tca cac ttc aaa caa ctt   144
Val Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu
        35                  40                  45

cat acc cca aca aat tgg ctc att cat tcc atg gcc act gtg gac ttt   192
His Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe
    50                  55                  60

ctt ctg ggg tgt ctg gtc atg cct tac agt atg gtg aga tct gct gag   240
Leu Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu
65                  70                  75                  80

cac tgt tgg tat ttt gga gaa gtc ttc tgt aaa att cac aca agc acc   288
His Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr
                85                  90                  95

gac att atg ctg agc tca gcc tcc att ttc cat ttg tct ttc atc tcc   336
Asp Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser
            100                 105                 110

att gac cgc tac tat gct gtg tgt gat cca ctg aga tat aaa gcc aag   384
Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys
        115                 120                 125

atg aat atc ttg gtt att tgt gtg atg atc ttc att agt tgg agt gtc   432
Met Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val
    130                 135                 140

cct gct gtt ttt gca ttt gga atg atc ttt ctg gag cta aac ttc aaa   480
Pro Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys
145                 150                 155                 160

ggc gct gaa gag ata tat tac aaa cat gtt cac tgc aga gga ggt tgc   528
Gly Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys
                165                 170                 175

tct gtc ttc ttt agc aaa ata tct ggg gta ctg acc ttt atg act tct   576
Ser Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser
            180                 185                 190

ttt tat ata cct gga tct att atg tta tgt gtc tat tac aga ata tat   624
Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr
        195                 200                 205
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ctt atc gct aaa gaa cag gca aga tta att agt gat gcc aat cag aag   672
Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln Lys
    210                 215                 220

ctc caa att gga ttg gaa atg aaa aat gga att tca caa agc aaa gaa   720
Leu Gln Ile Gly Leu Glu Met Lys Asn Gly Ile Ser Gln Ser Lys Glu
225                 230                 235                 240

agg aaa gct gtg aag aca ttg ggg att gtg atg gga gtt ttc cta ata   768
Arg Lys Ala Val Lys Thr Leu Gly Ile Val Met Gly Val Phe Leu Ile
                245                 250                 255

tgc tgg tgc cct ttc ttt atc tgt aca gtc atg gac cct ttt ctt cac   816
Cys Trp Cys Pro Phe Phe Ile Cys Thr Val Met Asp Pro Phe Leu His
            260                 265                 270

tac att att cca cct act ttg aat gat gta ttg att tgg ttt ggc tac   864
Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val Leu Ile Trp Phe Gly Tyr
        275                 280                 285

ttg aac tct aca ttt aat cca atg gtt tat gca ttt ttc tat cct tgg   912
Leu Asn Ser Thr Phe Asn Pro Met Val Tyr Ala Phe Phe Tyr Pro Trp
    290                 295                 300

ttt aga aaa gca ctg aag atg                                      933
Phe Arg Lys Ala Leu Lys Met
305                 310
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<211> 311
<212> PRT
<213> Homo sapiens

<400> 124

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His Val Leu Asn Phe Gln Glu Leu Phe Phe Leu Val Phe Gly Val Ser
 1               5                  10                  15

Thr Leu Ile Val Val Phe Leu Met Val Leu Ile Ile Leu Thr Thr Leu
            20                  25                  30
Val Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu
        35                  40                  45
His Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe
    50                  55                  60
Leu Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu
65                  70                  75                  80
His Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr
                85                  90                  95
Asp Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser
            100                 105                 110
Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys
        115                 120                 125
Met Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val
    130                 135                 140
Pro Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys
145                 150                 155                 160
Gly Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys
                165                 170                 175
Ser Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser
            180                 185                 190
Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr
        195                 200                 205
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Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln Lys
    210                 215                 220
Leu Gln Ile Gly Leu Glu Met Lys Asn Gly Ile Ser Gln Ser Lys Glu
225                 230                 235                 240
Arg Lys Ala Val Lys Thr Leu Gly Ile Val Met Gly Val Phe Leu Ile
                245                 250                 255
Cys Trp Cys Pro Phe Phe Ile Cys Thr Val Met Asp Pro Phe Leu His
            260                 265                 270
Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val Leu Ile Trp Phe Gly Tyr
        275                 280                 285
Leu Asn Ser Thr Phe Asn Pro Met Val Tyr Ala Phe Phe Tyr Pro Trp
    290                 295                 300
Phe Arg Lys Ala Leu Lys Met
305                 310
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